

Appendix

Dynamics of Adaptive Microevolution of Hypermutable *Pseudomonas aeruginosa* during Chronic Pulmonary Infection in Patients with Cystic Fibrosis.

Hoboth C, Hoffmann R, Eichner A, Henke C, Schmoldt S, Imhof A, Heesemann J, Hogardt M.

CF-patients

CF-patients M, V, and P each suffered from chronic CF-lung disease and PA lung infection since several years. Patient M clinical characteristics: born 1967, exocrine pancreas insufficiency, history of chronic PA colonization since several years, although it was well-documented only since 1997 (no earlier data available), the patient refused to be listed for lung transplantation, death at the age of 34 due to respiratory insufficiency. Patient V clinical characteristics: born 1972, exocrine pancreas insufficiency, allergic bronchopulmonary aspergillosis, diabetes mellitus, chronic PA colonization documented since the age of 19, listed for lung transplantation, however, the patient died beforehand at the age of 30 due to respiratory insufficiency. Patient P clinical characteristics: born 1975, exocrine pancreas insufficiency, diabetes mellitus, chronic PA colonization since the age of 12, lung transplantation at the age of 28, the patient died 10 months later due to circulatory and respiratory failure with posttransplant bronchial stenoses (see also table 1).

Supporting Experimental Procedures

Micro-aerobic growth of *P. aeruginosa* (PA) in LB liquid culture

Due to the increasing evidence that the environment of CF-airways is micro-aerobic and rich in nutrients (decaying cell detritus) we chose LB-broth and low O₂-concentrations for this comparative proteome and transcriptome analysis [1,2]. To adhere to low O₂ tension PA is faced in vivo, we initially determined O₂-concentration of PA in vitro culture (batches of 250ml LB broth within 500ml flasks covered with aluminium foil to limit oxygen influx

under shaking to avoid nutrient or oxygen gradients). Strikingly, during PA growth the increase in cell density is accompanied by a rapid decrease of O₂ in the growth medium. When reaching late-logarithmic growth phase ($OD_{600} \geq 3$), oxygen is rapidly consumed approaching O₂-concentration below 1% (conferring hypoxic growth conditions, data not shown). Thus, O₂-concentrations in PA batch cultures harvested for subsequent proteome and transcriptome analysis at $OD_{600} > 3.0$ seem feasible to mimic micro-aerobic lifestyle of PA within CF-lung. Although it is not feasible to completely simulate complex growth conditions of the CF-lung (e.g. regarding the low but likely continuously repleted nitrate needed for anaerobic growth), the abundance of amino acids, peptides and nucleic acids of LB-broth (casein digest and autolysed yeast extract), the micro-aerobiosis and high cell densities seem to fit to the growth conditions of PA in the CF-mucus [3,4]. Therefore, nitrate was added to growth medium only for anaerobic control experiments in air-tight sealed flasks at concentrations 15mM or 50mM but not during micro-aerobic growth ([figure A1](#)). Not surprisingly, genes of major denitrification enzymes (NAR, NIR, NOR, N₂OR) were slightly decreased in the transcriptome under micro-aerobic growth in LB, probably because of the deficiency of nitrate that is needed to sufficiently up-regulate *nir/nar* genes (see [table A2](#)) [5].

Affymetrix *P. aeruginosa* GeneChip experiments

RNA of PA cultures ($OD_{600nm} \sim 3.5$; O₂-concentration < 1%) was isolated in triplicate from independent growth experiments using TRIzol (Invitrogen). Purified total RNA was treated with deoxyribonuclease to remove residual DNA. RNA preparations were checked for DNA contamination by PCR. Quality of RNA preparation and fragmentation was checked by denaturation gel electrophoresis. Synthesis of biotin-labeled cDNA (from 11µg RNA), hybridization, and scanning of *P. aeruginosa* GeneChip arrays was performed according to the manufacturer's instructions (Affymetrix). Data were normalized, and transcript-specific

gene expression levels were calculated, using rma [6,7] as implemented in R (R core team) and Bioconductor [8]. Differentially expressed genes were identified using the permutation-based method of Tusher (sam) as implemented in the "samr" R package [9,10]. To control for multiple testing, a false discovery rate (FDR) was calculated as the percentage of genes falsely detected as differentially expressed among all genes detected as differentially expressed [11]. The q-value is the lowest FDR at which the gene is called significant. Significant genes were identified at the most stringent q-value possible (<1%) and with a fold-change of ≥ 2 . Cluster analysis of differentially expressed genes was performed using uncentered Pearson's correlation as similarity metric on z-score transformed gene expression values and average linkage clustering [12]. The transcriptome analysis yielded a genome-wide analysis of both increased (\uparrow) and decreased (\downarrow) transcripts. Differentially expressed transcripts derived from the comparison of isogenic PA mutator and non-mutator isolates of patient M are summarized in [table A1](#) to [table A2](#) (raw transcriptome data are available from the

Gene	Expression	Omnibus	repository
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<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE10362>).

Proteome analysis

The comparative proteome analysis focussed on the quantification of protein spots which were significantly increased (\uparrow) in late mutator isolates (M_i , V_i , and P_i , i = index) as compared to proteome pattern of the earliest non-mutator M_1 , V_1 and P_4 of patient M, V, and P, respectively. Changes in protein amounts of lung-selected mutator strains should reflect alterations in expression of corresponding genes due to adaptive events that have been encountered by descending PA variants. The proteome of PA strains was separated into whole cell (WC), supernatant (SN) and surface-associated (SA) sub-proteomes prior to two-dimensional gel electrophoresis (2-DE) as described [13]. For proteome analysis PA was grown in LB to stationary phase ($OD_{600nm} \sim 3.0$). For preparation of WC lysate (WCL), 400ml

of culture was harvested (4300rpm; 4°C; 30min), bacterial cells were washed twice with 0.9% NaCl, once with Tris-HCl (50mM, pH 7.5) and resuspended in Tris-HCl (supplemented with Protease Inhibitor Cocktail, Roche). Cell lysis was performed by french press and cell debris was removed by centrifugation (15000rpm, 1h, 4°C). To improve isoelectric focusing of proteins, WCL was phenol-extracted as described [14]. The proteins were precipitated from aqueous phase with ice-cold acetone, sedimented by centrifugation (15000rpm; 20min; 4°C), washed with acetone and air-dried. Finally, approximately 10mg precipitate were solubilised in 200µl of lysis buffer: 9.5M urea, 2% (w/v) CHAPS, 0.8% Pharmalyte pH 3-10, 1% dithiothreitol (DTT), and 5mM Pefabloc. Supernatant proteins (SPs) were obtained from 1000ml-culture supernatant by precipitation with 20% (w/v) trichloroacetic acid at 4°C overnight. The precipitate was harvested by centrifugation (4°C, 4300rpm, 1.5h), washed twice with ethanol and once with acetone, dried, resolved and phenol-extracted to remove non-proteinaceous compounds. The protein pellet (approximately 100mg) was solubilised in 200µl membrane protein lysis buffer [1% (w/v) tetradecanoyl-amido-propyl-dimethyl-ammonio propane-sulfonate (ASB14), 2mM tributyl-phosphine, 7M urea, 2M thiourea, 0.8% (w/v) Pharmalyte 3-10] [15].

SA-proteins were enriched by acidic glycine extraction [16]. Bacterial cells of a 1000ml-culture were harvested by centrifugation, washed twice in 5mM Tris-HCl, pH 7.5 and resuspended (4g/100ml) in 0.2M glycine hydrochloride, pH 2.2. The suspension was stirred at 20°C for 15min and cells were removed by centrifugation. The supernatant was neutralized with NaOH to pH 7.0 and the protein extract was precipitated with a threefold volume of acetone at 20°C overnight. The precipitate was harvested by centrifugation (4°C; 12000rpm; 60min), washed four times with ethanol and once with acetone, dried thoroughly. The final pellet (approximately 10mg) was resuspended in 200µl membrane lysis buffer.

Two-dimensional gel electrophoresis (2-DE)

Isoelectric focusing (IF) was performed using immobilized pH gradient (IPG) strips (17cm, pH 3–10 NL, pH 4–7). Protein samples were mixed with rehydration solution: 8M urea, 2% (w/v) CHAPS, 15mM DTT and 0.5% (v/v) IPG-buffer pH 3-10 or pH 4-17 (Biorad), respectively, resulting in a final protein amount of 400µg protein in a volume of 350µl. The isoelectric focusing was performed by using IPG strips (BioRad) as described [17]. The IPG strips were rehydrated actively for 12h at 50V and focused for 3h at 8000V at 20°C under mineral oil. IPG strips were then incubated for 10min, in equilibration buffer I [6M urea, 30% w/v glycerol, 2% w/v SDS and 1% w/v DTT in 50mM Tris-HCl buffer, pH 8.8] followed by equilibration buffer II [6M urea, 30% w/v glycerol, 2% w/v SDS and 4% w/v iodacetamide in 50mM Tris-HCl buffer, pH 8.8]. After the equilibration step, the strips were transferred to a 12.5% SDS–PAGE gels for second dimension. Electrophoresis was initiated at 60mA for 2h and continued at 1W per Gel at 10°C for about 18h. Protein spots were visualized by staining with Coomassie brilliant blue G-250 as described [18].

Data analysis

Gels were scanned with a densitometric ImageScanner (BioRad) and analysed using the PDQuest 7.1 (BioRad) by considering only changes in spot intensity ≥ 2.0 -fold (increase: ≥ 2 -fold or decrease ≤ 0.5 -fold) as averaged over triplicate gels prepared from independent growth experiments. Protein spots fulfilling this criterion were subjected to in-gel tryptic digestion and analysed by peptide mass fingerprints using a MALDI-TOF mass spectrometer. Protein identification was done using the MASCOT™ (data not shown) search algorithm using sequences from the NCBI non redundant database (<http://www.ncbi.nlm.nih.gov/>) and *P. aeruginosa* Community Annotation Project (<http://www.pseudomonas.com/>). Identified proteins were arbitrarily numbered (e.g. CF1) and designated by protein abbreviation or PA-

number^P. The relative expression of each protein is given as the ratio of the protein amount P_n of tested isolates M_i (e.g. protein spot CF1 of isolate M25: P_1^{M25}) versus the corresponding spot CF1 of isolate M1 (P_1^{M1} ; that is P_1^{M25}/P_1^{M1} and in general $P_n^{M_i}/P_n^{M1}$) as calculated by PDQuest software from triplicate gels. Full names and expression levels of identified proteins are listed in manuscript table 1 (spots CF1-CF61; WC lysate) and Appendix [table A3](#) (SN protein spots: CF62 to CF81 and SA protein spots: CF82 to CF104). PA proteome of early non-mutator/late mutator pair of patient V and patient P were analyzed accordingly (table A4 and A5).

Functional classification of PA genes/proteins was performed according to available annotations and predictions from orthologous relationships by comparative genomics (<http://www.ncbi.nlm.nih.gov/COG>). Data were mapped to metabolic pathways based on the Kyoto Encyclopedia of Genes and Genomes (KEGG) (<http://www.genome.jp/kegg>).

Quantification of selected transcripts by Reverse Transcription real-Time PCR

Quantitative RT-PCR of transcripts of genes *oprF*, *ampC*, *aotJ*, *arcD*, *azu*, *ccpR*, PA0119 and *anr* was used to provide independent verification of microarray/proteome results or to check the individual transcription level during variable growth conditions or among the entire set of sequential isolates of patient M. Briefly, total cellular RNA was isolated in triplicate using TRIzol (Invitrogen). RNA preparations for RT-PCR were independent from those used for array hybridizations. After random hexamer-primed first-strand cDNA synthesis (Superscript II, Invitrogen), real-time PCR was performed in a 7500 Fast RT-PCR system using gene specific primers and TaqMan probes selected via Primer Express software (Applied Biosystems) using an initial polymerase activation step at 95°C for 10min followed by 45 cycles of 15sec at 95°C for denaturation and 1 min at 60°C for annealing and extension. Gene expression levels were recorded relative to the *rpoD* housekeeping gene as: $E = 2^{-\Delta CT}$ ($E =$

gene expression value, ΔCT = difference in crossing points between *rpoD* and target genes). Relative expression of 'housekeeping genes' *rpoD* versus that of DNA gyrase subunit B (*gyrB*) was determined for control. All PCR experiments were performed in triplicate, and SDs were calculated and displayed as error bars. For graphical display, the maximum gene expression value in every graph was given an arbitrary value of 10, and the remaining values and standard deviations were scaled accordingly, graphwise.

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Table A1: Differentially expressed transcripts derived from the comparison of a set of isogenic sequential *P. aeruginosa* mutator (M13/M22/M25/M26) and non-mutator isolates (M1/M9/M11/M23) of patient M (data are summarized in [figure A2](#)).

Table A2: Differentially expressed transcripts derived from the comparison of early *P. aeruginosa* non-mutator isolate M1 of patient M with its descended late mutator isolates M25, M26 (data are summarized in manuscript figure 1).

Table A3: List of *P. aeruginosa* supernatant (SN; CF 62 to CF 81) and surface-associated (SA; CF 82 to CF 104) proteins that were found to be differentially expressed by a factor more than 2 among sequential PA isolates of patient M as compared to earliest non-mutator isolate M1. *P. aeruginosa* strain PAO1 was included as a control. Symbol * indicates that from the same protein (P) more than one spot was identified by MALDI-MS. The relative protein expression among patient M isolates is indicated by the ratio P_n^{Mi}/P_n^{M1} of protein spot numbers (n) of isolates M13, M20, M23 and M25 (indicated by Mi) and the corresponding protein spot numbers of isolate M1 (P_n^{M1}) as determined by 2-DE software PDQuest (BioRad) (2-DE displays are not provided). For isolate M13 and M20 we were not able to prepare sufficient SA protein amounts by acidic glycine extraction for 2-DE analysis (n.d. not determined).

Table A4: Comparative analysis of the *P. aeruginosa* proteomes of early non-mutator and late mutator pair of patient V and patient P. Isolates P24 (*mutS*) versus P4 ($MutS^+$) and isolate V43 (*mutS*) versus V1 ($MutS^+$) were analyzed, respectively (2-DE displays are not provided in Appendix). Analysis was focused on whole cell lysate proteins that were found to be

differentially expressed (increase: ≥ 2 -fold or decrease ≤ 0.5 -fold) between mutator/non-mutator isolates of patient M. The relative protein expression of isogenic PA pairs was calculated by ratios P_n^{V43}/P_n^{V1} (patient V), P_n^{P4}/P_n^{P24} (patient P) and indicated by arrows (absolute ratios are listed in [table A5](#)). For comparison the change in protein amounts for isogenic patient M pairs as determined by the ratios P_n^{M25}/P_n^{M1} and P_n^{M26}/P_n^{M1} (patient M) from triplicate gels using software PDQuest (BioRad) is shown. For proteins that formed more than one spot relative expression ratios were calculated from the total amount of scattered proteins (as determined by MALDI) by summing up the amounts of individual spot quantities.

Table A3:

Supernatant proteins								
CF spot Number (n) ^a	Ratio ^b : P _n ^{Mi} /P _n ^{M1}					protein function	gene	PA no.
	PAO1	M13	M20	M23	M25			
62	1,81	1,92	1,33	2,14	3,72	arginine/ornithine binding protein AotJ	<i>aotJ</i>	0888
63	1,17	2,39	1,39	1,06	2,22	branched-chain amino acid transport protein BraC	<i>braC</i>	1074
64*	4,3	0	0	0,12	0	flagellar capping protein FliD	<i>fliD</i>	1094
	5,2	0,06	0,03	0,57	0			
65	400,3	0,01	0,01	1,9	0,01	flagellin type B	<i>fliC</i>	1092
66	0,88	1,33	1,34	1,84	2,08	hypothetical protein	/	3313
67	1,05	0,34	0,26	0,34	0,18	hypothetical protein	/	0754
68	0,52	0,11	0	0,26	0,46	conserved hypothetical protein	/	3309
69	0,3	0,03	0,02	0,12	0,2	conserved hypothetical protein	/	3785
70	1,92	6	15,67	2,67	5,37	PhoP/Q and low Mg ²⁺ inducible outer membrane protein H1 precursor	<i>oprH</i>	1178
71*	0	9,86	1,33	0,71	2,87	GroEL protein	<i>groEL</i>	4385
	0	0,51	2,93	0,24	2,14			
	3,05	0,12	1,52	0,71	50,7			
72*	0,93	0,79	1989,2 ₅	1526,61	1095,05	beta-lactamase precursor	<i>ampC</i>	4110
	0,93	0,79	439,86	141,77	450,84			
	0,93	0,79	4122,0 ₄	3733,22	1855,99			
	0,93	0,79	938,3	597,56	1907,45			
73	216	82,9	129,2	93	277,9	dihydrolypoamide dehydrogenase 3	<i>lpd3</i>	4829
74	5,31	3,2	3,82	2,47	5,6	trigger factor	<i>tig</i>	1800
75	0,93	1,5	1,97	2,57	3,28	ATP synthase B chain	<i>atpF</i>	5558
76	2,73	4,24	2,40	1,66	2,52	arginine deiminase	<i>arcA</i>	5171
77*	4,67	19,26	12,79	18,02	3,35	azurin precursor	<i>azu</i>	4922
	1,91	2,92	0,87	2,25	1,92			
78*	0,52	1,81	2,1	0,66	2,59	inosine-5'-monophosphate dehydrogenase	<i>guaB</i>	3770
	1,98	2,47	2,4	1,76	3,24			
80	1,34	1,69	1,55	1,95	3,14	single-stranded DNA-binding protein	<i>ssb</i>	4232
79	0,17	0,47	0,32	0,61	0,52	probable ribosomal protein L25	/	4671
81	1697,5	0	0	0	0	elastase LasB	<i>lasB</i>	3724
Surface-associated proteins								
82*	1,01	n.d.	n.d.	0	14,13	major porin and structural outer membrane porin OprF precursor	<i>oprF</i>	1777
	1,07	n.d.	n.d.	0,04	4,76			
83*	0,01	n.d.	n.d.	0,28	2,94	major porin and structural outer membrane porin OprF precursor; c-terminus	<i>oprF</i>	1777
	2,58	n.d.	n.d.	0,98	16,3			
	0,02	n.d.	n.d.	0,01	4,38			
84	0,46	n.d.	n.d.	0,02	2,33	outer membrane protein OprG precursor	<i>oprG</i>	4067
85	0,89	n.d.	n.d.	1,6	0,07	probable TonB-dependent receptor	/	5505
86 105*	1,22	n.d.	n.d.	2,44	0,44	probable binding protein component of ABC transporter	/	1342
87	1,7	n.d.	n.d.	1,51	2,43	periplasmic chaperone LolA	<i>lolA</i>	2614
88	0,12	n.d.	n.d.	0,57	0,15	peptidoglycan associated lipoprotein OprL precursor	<i>oprL</i>	0973

89	0,53	n.d.	n.d.	5,96	1,09	serine protease MucD precursor	<i>mucD</i>	0766
90	0,35	n.d.	n.d.	3,98	5,25	conserved hypothetical protein	/	4739
91*	0	n.d.	n.d.	0	7,22	hypothetical protein	/	0388
	1,18	n.d.	n.d.	1,16	2,05			
92	0,77	n.d.	n.d.	30,18	89,21	hypothetical protein	/	0315
94	0,02	n.d.	n.d.	0,01	11,97	conserved hypothetical protein	/	4460
93	4,22	n.d.	n.d.	4,42	2,79	hypothetical protein	/	2659
95	1,06	n.d.	n.d.	0,6	3,3	conserved hypothetical protein	/	4453
96	2,12	n.d.	n.d.	2,92	2,51	hypothetical protein	/	5233
97	0,02	n.d.	n.d.	1,55	0,26	secreted factor PasP	<i>pasP</i>	0423
96	2,12	n.d.	n.d.	2,92	2,51	hypothetical protein	/	5233
97	0,02	n.d.	n.d.	1,55	0,26	secreted factor PasP	<i>pasP</i>	0423
98	58,89	n.d.	n.d.	26,59	0,72	conserved hypothetical protein	/	3785
99	0,14	n.d.	n.d.	2,12	0	hypothetical protein	/	0946
100	0,12	n.d.	n.d.	2,27	8,04	GroES protein	<i>groES</i>	4386
101*	1,26	n.d.	n.d.	1,53	3,7	azurin precursor	<i>azu</i>	4922
	2,85	n.d.	n.d.	3,4	6,16			
102*	3904,88	n.d.	n.d.	100,9	0,43	flagellin type B	<i>fliC</i>	1092
	1405,11	n.d.	n.d.	80,75	1,3			
	1289,7	n.d.	n.d.	0	0			
103*	36,97	n.d.	n.d.	0,01	0,01	flagellar capping protein FliD	<i>fliD</i>	1094
104*	0	n.d.	n.d.	1947,9	870,4	beta-lactamase precursor	<i>ampC</i>	4110
	0	n.d.	n.d.	7295,7	5462,2			
	0	n.d.	n.d.	5223,6	3847,4			
	0	n.d.	n.d.	5341,6	2774,3			

Table A3 continued

Note:

- Symbol * indicated that from the same protein (P) more than one spot was identified by MALDI-MS.
- The relative protein expression in comparison to the earliest non-mutator isolate M1 ($MutS^+$) is indicated by the ratio P_n^{Mi}/P_n^{M1} of respective protein spot numbers (n) of isolates M13 (*mutS*), M20 (*mutS*), M23 ($MutS^+$), M25 (*mutS*), indicated by M_i , and the corresponding protein spot of isolate M1 (P_n^{M1}) as determined by 2-DE software PDQuest (BioRad, 0 = spot not detected/incalculable). *P. aeruginosa* strain PAO1 was included as a control.

Table A4: Comparison of the proteomes of end-stage PA isolates of patient M, V and P^a

CF spot number (n)	Relative expression ratios ^b				protein function	gene	PA no.
	$\frac{P_n^{M26}}{P_n^{M1}}$	$\frac{P_n^{M25}}{P_n^{M1}}$	$\frac{P_n^{P24}}{P_n^{P4}}$	$\frac{P_n^{V43}}{P_n^{V1}}$			
1	-	↑	↑	↑	binding protein RbsB of ABC ribose transporter	<i>rbsB</i>	1946
2	↑	↑	↑	↑	arginine/ornithine binding protein AotJ	<i>aotJ</i>	888
3	↑	↑	↑	↓	probable lysine-arginine-ornithine-binding periplasmic protein	/	5153
4	-	↑	↑	↑	probable lysine-arginine-ornithine-binding periplasmic protein	/	1260
5	↑	↑	↑	↑	periplasmic branched-chain amino acid transport protein BraC	<i>braC</i>	1074
6	↑	↑	↑	↑	Polyamine transport protein SpuD	<i>spuD</i>	300
7	↑	-	↑	↓	outer membrane porin OprF	<i>oprF</i>	1777
8	↓	↓	↓	↓	outer membrane porin OprD	<i>oprD</i>	958
9	-	↑	↑	↑	fructose-1,6-bisphosphate aldolase	<i>fda</i>	555
10	-	↑	-	-	Adenylate kinase	<i>adk</i>	3686
11	-	↑	↑	↑	azurin precursor	<i>azu</i>	4922
12	-	↑	↑	↑	cytochrom c551 peroxidase precursor	<i>ccpR</i>	4587
13	-	-	↓	↑	3-isopropylmalate dehydratase small subunit	<i>leuD</i>	3120
14	-	↑	↓	↑	imidazoleglycerol-phosphate synthase, cyclase subunit	<i>hisF1</i>	5140
15	-	↑	↑	↑	arginine deiminase	<i>arcA</i>	5171
16	↑	↑	↑	-	carbamate kinase	<i>arcC</i>	5173
17	-	↑	↑	↑	probable biotin-dependent carboxylase	/	2888
18	↑	↑	↓	↑	acyl carrier protein	<i>acpP</i>	2966
19	-	↑	↑	↑	acetyl-CoA carboxylase	<i>accB</i>	4847
20	↑	↑	↓	-	inorganic pyrophosphatase	<i>ppa</i>	4031
21	-	↑	-	-	thioredoxin	<i>trxA</i>	5240
22	-	↑	↑	-	succinyl-CoA synthetase beta chain	<i>sucC</i>	1588
23	↓	-	↑	↑	glutaminase-asparaginase	<i>ansB</i>	1337
24	-	-	↑	-	dihydrolipoamid dehydrogenase 3	<i>lpdG</i>	4829
25	↑	↑	-	↑	malate synthase G	<i>glcB</i>	482
26	-	↑	↓	↓	ATP synthase B chain	<i>atpF</i>	5558
27	↑	↑	-	-	ATP synthase H chain	<i>atpH</i>	5557
28	-	↑	↑	↑	pyridoxamin 5'-phosphate oxidase	<i>pdxH</i>	1049
29	↑	↑	-	↑	nitrogen regulatory protein P-II 2	<i>glnK</i>	5288
30	-	↓	↓	↓	probable CoA-transferase, subunit A	<i>atoD</i>	1999
31	↓	↓	↓	↓	acetyl-CoA acetyltransferase	<i>atoB</i>	2001
32	-	↑	↓	-	hypothetical protein	/	318
33	-	↑	↑	↑	hypothetical protein	/	2575
34	↑	↑	-	↑	hypothetical protein	/	388
35	↑	↑	-	-	hypothetical protein	/	3440

CF spot number (n)	Relative expression ratios ^b				protein function	gene	PA no.
	P_n^{M26} / P_n^{M1}	P_n^{M25} / P_n^{M1}	P_n^{P24} / P_n^{P4}	P_n^{V43} / P_n^{V1}			
36	↓	↓	-	↑	hypothetical protein	/	1677
37	↓	↓	↓	↓	hypothetical protein	/	5178
38	-	-	↑	-	hypothetical protein	/	3309
39	-	↑	↑	↑	hypothetical protein	/	5339
40	↑	↑	↓	↓	glutathione peroxidase	<i>btuE</i>	838
41	-	↓	-	↑	superoxide dismutase	<i>sodB</i>	4366
42	↓	↑	↑	↑	kynurenine formamidase	/	2081
43	↓	↓	↓	↓	bakterioferritin A	<i>bfrA</i>	4235
44	↓	↓	↓	↓	katalase	<i>katA</i>	4236
45	-	↓	↓	-	alkyl hydroperoxide reductase subunit C	<i>ahpC</i>	139
46	-	-	-	↑	probable peroxidase	<i>tsaA</i>	3529
47	-	↓	↓	↓	heat-shock protein IbpA	<i>ibpA</i>	3126
48	-	↑	↑	-	peptidyl-prolyl cis-trans isomerase B	<i>ppiB</i>	1793
49	-	-	-	↓	GroEL protein	<i>groEL</i>	4385
50	-	-	-	↓	trigger factor	<i>tig</i>	1800
51	↑	↑	↑	↑	30S ribosomal protein S6	<i>rpsF</i>	4935
52	-	-	-	-	probable ribosomal protein L25	/	4671
53	-	↑	↓	-	transcription elongation factor GreA	<i>greA</i>	4755
54	↑	↑	↑	-	50S ribosomal protein L7/L12	<i>rpIL</i>	4271
55	-	-	-	↓	elongation factor Ts	<i>tsf</i>	3655
56	↑	↑	↑	-	elongation factor Tu	<i>tufA</i>	4265
57	-	↑	↑	↑	inosine-5'-monophosphate dehydrogenase	<i>guaB</i>	3770
58	↑	↑	↓	-	twitching motility protein PilH	<i>pilH</i>	409
59	↓	↓	↓	↓	flagellin type B	<i>fliC</i>	1092
60	↓	↓	↓	↓	UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate-D-alanyl-D-alanyl ligase	<i>murF</i>	4416
61	-	↓	↓	-	cell division protein FtsZ	<i>ftsZ</i>	4407

Table A4 continued

Notes:

- Interproteome comparison of changes of protein spots CF1-CF61 that were found to be differentially expressed between mutator/non-mutator isolates of patient M with those from respective WC lysate subproteomes of an early non-mutator and late mutator pair of patient V and patient P, respectively. PA isolate P24 (mutator) versus P4 and isolate V43 (mutator) versus V1 were analyzed.
- The relative protein expression among isogenic PA isolates was calculated by ratios P_n^{V43}/P_n^{V1} , P_n^{P4}/P_n^{P24} and ratios P_n^{M25}/P_n^{M1} and P_n^{M26}/P_n^{M1} is indicated by arrows (upregulation ↑, downregulation ↓, minus indicated no significant change in protein expression; absolute corresponding ratios are shown in [table A5](#)) For proteins that formed more than one spot relative expression ratios were calculated from the total amount of scattered proteins (as determined by MALDI) by summing up the amounts of individual spot quantities.

Table A5:

CF spot number (n)	P_n^{M26} / P_n^{M1}	P_n^{M25} / P_n^{M1}	P_n^{P24} / P_n^{P4}	P_n^{V43} / P_n^{V1}	protein function	gene	PA no.
1	1,07	2,06	60,72	67,67	binding protein RbsB of ABC ribose transporter	<i>rbsB</i>	1946
2	2,08	3,38	37,8	89,57	arginine/ornithine binding protein AotJ	<i>aotJ</i>	888
3	2,92	3,15	2,56	0,50	probable lysine-arginine-ornithine-binding periplasmic protein	/	5153
4	1,15	2,4	120,73	13,98	probable lysine-arginine-ornithine-binding periplasmic protein	/	1260
5	2,58	2,17	719,67	4,34	periplasmic branched-chain amino acid transport protein BraC	<i>braC</i>	1074
6	3,05	4,97	2,65	2,68	Polyamine transport protein SpuD	<i>spuD</i>	300
7	5,2	1,8	7,3	0,43	outer membrane porin OprF	<i>oprF</i>	1777
8	0	0	/	0,27	outer membrane porin OprD	<i>oprD</i>	958
9	1,82	2,28	86,55	4,19	fructose-1,6-bisphosphate aldolase	<i>fda</i>	555
10	0,99	2,02	0,53	0,88	Adenylate kinase	<i>adk</i>	3686
11	1,3	2,9	6,4	5,4	azurin precursor	<i>azu</i>	4922
12	1,4	3,6	2,1	28,5	cytochrom c551 peroxidase precursor	<i>ccpR</i>	4587
13	1,0	1,2	0,5	4,8	3-isopropylmalate dehydratase small subunit	<i>leuD</i>	3120
14	1,65	2,27	/	18,51	imidazoleglycerol-phosphate synthase, cyclase subunit	<i>hisF1</i>	5140
15	1,6	2,0	9,6	8,2	arginine deiminase	<i>arcA</i>	5171
16	2,1	4,3	85,9	1,5	carbamate kinase	<i>arcC</i>	5173
17	1,77	5,22	3,42	867,99	probable biotin-dependent carboxylase	/	2888
18	104,22	159,77	/	6,78	acyl carrier protein	<i>acpP</i>	2966
19	1,99	2,08	150,35	10,54	acetyl-CoA carboxylase	<i>accB</i>	4847
20	2,5	2,6	0,2	1,41	inorganic pyrophosphatase	<i>ppa</i>	4031
21	1,65	2,43	0,95	1,06	thioredoxin	<i>trxA</i>	5240
22	1,3	2,1	165,37	0,63	succinyl-CoA synthetase beta chain	<i>sucC</i>	1588
23	0,5	1,7	2,2	5,2	glutaminase-asparaginase	<i>ansB</i>	1337
24	1,8	1,75	2,08	0,65	dihydrolipoamid dehydrogenase 3	<i>lpdG</i>	4829
25	2,0	2,2	1,9	4,3	malate synthase G	<i>glcB</i>	482
26	1,2	2,17	/	0,34	ATP synthase B chain	<i>atpF</i>	5558
27	3,15	2,53	0,66	1,76	ATP synthase H chain	<i>atpH</i>	5557
28	0,91	2,45	216,83	4,23	pyridoxamin 5'-phosphate oxidase	<i>pdxH</i>	1049
29	4,22	5,54	1,97	81,19	nitrogen regulatory protein P-II 2	<i>glnK</i>	5288
30	1,26	0,35	0,47	0,48	probable CoA-transferase, subunit A	<i>atoD</i>	1999
31	0,49	0,42	0	0,42	acetyl-CoA acetyltransferase	<i>atoB</i>	2001
32	1,73	3,13	0,37	1,14	hypothetical protein	/	318
33	1,6	2,57	149,34	110,93	hypothetical protein	/	2575
34	8,31	14,4	1,46	7,36	hypothetical protein	/	388
35	86,38	180,34	1,16	1,03	hypothetical protein	/	3440
36	0,37	0,42	1,2	2,08	hypothetical protein	/	1677
37	0,3	0,31	0,37	0,00	hypothetical protein	/	5178
38	1,4	0,8	2,26	1,11	hypothetical protein	/	3309

CF spot number (n)	P_n^{M26} / P_n^{M1}	P_n^{M25} / P_n^{M1}	P_n^{P24} / P_n^{P4}	P_n^{V43} / P_n^{V1}	protein function	gene	PA no.
39	1,78	2,09	6,65	2,94	hypothetical protein	/	5339
40	59,54	115,71	/	/	glutathione peroxidase	<i>btuE</i>	838
41	0,7	0,4	1	243,6	superoxide dismutase	<i>sodB</i>	4366
42	0,38	9,89	9,94	103,97	kynurenine formamidase	/	2081
43	0,12	0	/	0,00	bakterioferritin A	<i>bfrA</i>	4235
44	0,01	0,36	/	/	katalase	<i>katA</i>	4236
45	0,71	0,49	0,4	0,8	alkyl hydroperoxide reductase subunit C	<i>ahpC</i>	139
46	0,9	0,9	0,54	2,9	probable peroxidase	<i>tsaA</i>	3529
47	0,52	0,04	/	/	heat-shock protein IbpA	<i>ibpA</i>	3126
48	1,65	2,62	2	1,74	peptidyl-prolyl cis-trans isomerase B	<i>ppiB</i>	1793
49	0,82	0,8	0,53	0,35	GroEL protein	<i>groEL</i>	4385
50	1,81	1,07	0,95	0,32	trigger factor	<i>tig</i>	1800
51	2,2	5,26	29,63	14,5	30S ribosomal protein S6	<i>rpsF</i>	4935
52	1,56	1,88	0,93	0,98	probable ribosomal protein L25	/	4671
53	1,86	2,15	0,27	0,89	transcription elongation factor GreA	<i>greA</i>	4755
54	2	4,37	3,25	0,53	50S ribosomal protein L7/L12	<i>rplL</i>	4271
55	1,0	0,9	0,95	0,3	elongation factor Ts	<i>tsf</i>	3655
56	5,7	2,5	2442,39	1,16	elongation factor Tu	<i>tufA</i>	4265
57	0,51	3,06	5,74	4,7	inosine-5'-monophosphate dehydrogenase	<i>guaB</i>	3770
58	2,58	2,6	0,09	0,91	twitching motility protein PilH	<i>pilH</i>	409
59	0,2	0,0	0	/	flagellin type B	<i>fliC</i>	1092
60	0,28	0,46	/	0,00	UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate-D-alanyl-D-alanyl ligase	<i>murF</i>	4416
61	0,52	0,24	0,25	0,72	cell division protein FtsZ	<i>ftsZ</i>	4407

Table A5 continued:

LIST OF APPENDIX FIGURES

Figure A1: RT-PCR analyses of *P. aeruginosa* transcripts of genes encoding outer membrane protein F (*oprF*), azurin (*azu*) putative dicarboxylate transporter PA01119 among sequential patient M isolates M1 (non-mutator, □) and M25/M26 (mutators, ▨) respectively, using different growth conditions (micro-aerobic growth versus anaerobic growth using LB broth supplemented either with 15mM or 50mM nitrate as indicated). Expression of target genes is shown relative to that of ‘housekeeping gene’ *rpoD* encoding sigma factor RpoD. Independent of the addition of nitrate transcripts of *oprF*, *azu* and PA0119 were constitutively increased in mutator isolates M25/M26 suggesting constitutive up-regulation. In contrast, as to be expected in response to anaerobic growth conditions expression level of *azu* increased in early non-mutator M1. For comparison the relative expression of ‘housekeeping gene’ *gyrB* (encoding DNA gyrase subunit B) versus that of ‘housekeeping gene’ *rpoD* that showed no significant difference between non-mutator M1 and mutators M25/M26 is included as control.

Figure A2: Functional classification of genes with statistically significant increase or decrease in mRNA level (a total of 260 genes, genes are listed in [table A1](#)) when comparing a set of sequential mutator strains (M13/M22/M25/M26) with a set of isogenic *P. aeruginosa* non-mutator strains (M1/M9/M11/M23) of patient M using Affymetrix *P. aeruginosa* GeneChips. Data for 171 genes are shown, while hypothetical, unclassified, unknown proteins (40 up-regulated and 49 down-regulated) were not included.

Figure A3: Comparative 2-DE analysis and corresponding gel regions A-F of whole cell (WC) lysate proteins of sequential *P. aeruginosa* patient M non-mutator (MutS⁺) and mutator (*mutS*) isolates: M1 (MutS⁺), M9 (MutS⁺), M13 (*mutS*), M20 (*mutS*), M23 (MutS⁺), M25

(*mutS*), M26 (*mutS*) and *P. aeruginosa* PAO1, included as control, are shown. Proteins differentially expressed by a factor more than 2 based on the analysis of three different 2-DE-gels using PDQuest software (BioRad) are shown. CF spot numbers correspond to those of manuscript table 1 and PA numbers to those available from the *Pseudomonas* genome project (<http://www.pseudomonas.com>). Comparative 2-DE gel regions of supernatant (SN) and surface-associated (SA) proteins of sequential *P. aeruginosa* patient M non-mutator and mutator isolates are not shown. For isolate M13 and M20 we were not able to prepare sufficient SA protein amounts for 2-DE analysis by acidic glycine extraction. SA and SN proteins CF62-CF104 are differentially expressed by a factor more than 2 based on the analysis of three different 2-DE-gels are listed in [table A3](#).

Figure A4: Significant quantitative changes in transcripts of enzymes involved in aromatic compound metabolism of adapted end-stage *P. aeruginosa* mutator isolates M25/M26 of patient M as compared to early non-mutator isolate M1 (strikingly only decreased ↓ transcripts (T) were found; depicted in green). These transcripts include those of (i) *pcaH*↓ and *pchG*↓ encoding protocatechuate 3,4-dioxygenase a catechol dioxygenases that allow PA to use aromatic compounds by catalyzing the aromatic ring-opening step, (ii) PA0226↓, PA0227↓ (probable 3-oxoacid CoA transferase), *pcaF*↓ (beta-ketoadipyl CoA thiolase, PA0228↓) and the adjacent gene *pcaK*↓ (PA0235↓) encoding a 4-hydroxybenzoate transporter (PA0226↓-PA0231↓). PcaF putatively acts at the end of pathways for the degradation of protocatechuate from benzoate and related compounds. (iii) PA5410↓ encoding a probable aromatic ring hydroxylating dioxygenase, (iv) several genes of a large gene cluster, namely *catA*↓ (PA2507) encoding a putative catechol 1,2-dioxygenase, that catalyzes the oxygen-dependent ring-cleavage of catechol to muconic acid, *catC*↓ (muconolactone isomerase), *catB*↓ (muconate cycloisomerase) participating in beta-ketoadipate pathway that results in the

degradation of catechol to β -ketoadipate. Catechol in turn is an intermediate in the catabolism of different aromatic compounds such as anthranilate (*antA*↓ (PA2512↓), *antB*↓, *antC*↓ encoding a dioxygenase converting anthranilate to catechol, (v) PA2517↓ PA2518↓ encoding toluate-dioxygenase an aromatic-ring-hydroxylating dioxygenase, PA2085↓ encoding putative aromatic ring-hydroxylating dioxygenase and PA2086↓ a probable hydrolase, (vi) PA2098↓ encoding putative esterase/deacetylase acting during aromatic compound catabolism and *vanA*↓ (PA4904) encoding the oxygenase subunit of vanillate O-demethylase that converts vanillate into protocatechuate, and (vii) *soxB*↓ (PA5416), *soxD*↓, *soxA*↓ encoding three subunits of a putative heterotetrameric sarcosine oxidases catalyzing the oxygen-dependent demethylation of sarcosine.

Figure A5: Adapted metabolic pathways of end-stage *P. aeruginosa* isolates of patient M. Significant quantitative changes in transcripts and/or proteins amounts of genes involved in (A) Entner-Doudoroff pathway and (B) nucleic acid/nucleotide metabolism are shown. Decreased (depicted in green) and increased (depicted in red). Changes in protein amounts (P) or transcripts (T) of mutators M25/M26 as compared to non-mutator M1 are indicated.

(A) Entner-Doudoroff pathway: transcripts or proteins of Entner-Doudoroff pathway were widely unchanged, except gluconate transporter (PA2322↓), phosphoglycerate kinase (*pgk*↑) and phosphoenolpyruvate synthase (*ppsA*↑), that catalyze the synthesis of phosphoenolpyruvate (which e.g. may be carboxylated by phosphoenolpyruvate carboxylase (*ppc*↑) to oxalacetate), and proteins/transcripts of descending pyruvate dehydrogenase (*aceE*↑, *aceF*↑, *lpdG*↑/LpdG↑). In contrast, transcripts of PA3415/PA3417 encoding an alternative pyruvate dehydrogenase were decreased.

(B) Nucleic acid/nucleotide metabolism: in mutators M25/M26 the expression of genes or proteins of purine base metabolism were found to be altered, including an increase in: (i)

transcripts of genes involved in the biosynthesis of purines from 5'-phospho-ribose-1'-pyrophosphate (*purC*↑, *purL*↑, *purF*↑), and (ii) transcripts/proteins of the purine salvage pathway for utilization of preformed purine (*adk*↑, adenylate kinase; *guaA*, guanosine monophosphate synthase; *guaB*↑/GuaB↑, inosine monophosphate dehydrogenase; *purA*↑, adenylosuccinate synthetase; *purB*↑, adenylosuccinate lyase; PA3970↑, adenosine monophosphate nucleosidase). In contrast, differences in the expression of genes involved in pyrimidine metabolism were less distinctive (PA5541↓ encoding dihydroorotase was decreased). Interestingly, the transcript of *rnk*↑ encoding the positive regulator of nucleoside diphosphate kinase Ndk but not Ndk itself (indicated by the symbol #) and that of *pnp*↑ encoding polyribonucleotide nucleotidyltransferase were found to be increased (both targeting purine and pyrimidine nucleosides). Ndk provides nucleoside triphosphates for nucleic acid synthesis, while Pnp catalyzes the phosphorolysis reaction of RNA to nucleoside diphosphates during RNA degradation and biosynthesis. These data are conclusive with an increased turnover of nucleic acids/nucleotides in PA isolates M25/M26. DNA polymerase III (*dnaN*↑, *dnaX*↑, *holC*↑) and RNA polymerase (*rpoA*↑, *rpoC*↑) were found to be increased as described in results. Beside this, also several changes (not depicted in figure A5) in the expression of genes involved in transcription and translation were found: Interestingly, the expression level of components of the ribosomal 50S (proteome: L7, L11, L12, L18, L25, transcriptome: L1, L7, L12, L17, L19, L20, L24, L25, L31, L36) and 30S (proteome: S6, transcriptome: S6, S13, S14, S15, S18) subunit were increased. Moreover, transcription elongation factor GreA↑, translation elongation factors EF-Tu↑/EF-Ts↑, transcripts of DNA polymerase III (*dnaN*↑, *dnaX*↑, *holC*↑), translation initiation factor IF-2, and RNA polymerase (*rpoA*↑, *rpoC*↑) were quantitatively increased including numerous transcripts of aminoacyl-tRNA-synthetases (*ileS*↑, *cysS*↑, *glnS*↑, *argS*↑, *pheT*↑, *alaS*↑, *serS*↑, *thrS*↑, *aspS*↑, *hisS*↑, *glyS*↑). Since under starvation bacteria typically down-regulate rRNA-synthesis and

ribosome production, these results may reflect nutritional-rich conditions of CF-mucus and are in good agreement with the increase of transcripts of nucleic acid/nucleotide metabolism.

Figure A6: RT-PCR analyses of PA genes encoding outer membrane protein OprF (*oprF*), arginine/ornithine binding protein AotJ (*aotJ*), ANR-regulated cytochrome C₅₅₁ peroxidase (*ccpR*), azurin (*azu*) and (*arcD*) as well as anaerobic regulator ANR (*anr*) of early non-mutator/end-stage mutator pairs M1/M26; V1/V43, and P4/P24. PA non-mutators (□) and mutators (■) are indicated. RT-PCR for the gene of DNA gyrase subunit B (*gyrB*) was shown for control. RNA of PA cultures was harvested in triplicate from independent growth experiments at OD_{600nm} ~ 3.5; (O₂-concentration < 1%) and in case of *anr*-gene in addition at OD_{600nm} ~ 1.0; (O₂-concentration ~ 20%). In case of P4/P24 with used *arcD* primers and probe no PCR-amplicon could be detected. An arbitrary value of 10 was given for the maximum gene expression of each gene and patient, respectively, and the remaining values and standard deviations were scaled accordingly.

Appendix figures **A1-A6:**

Figure A1:

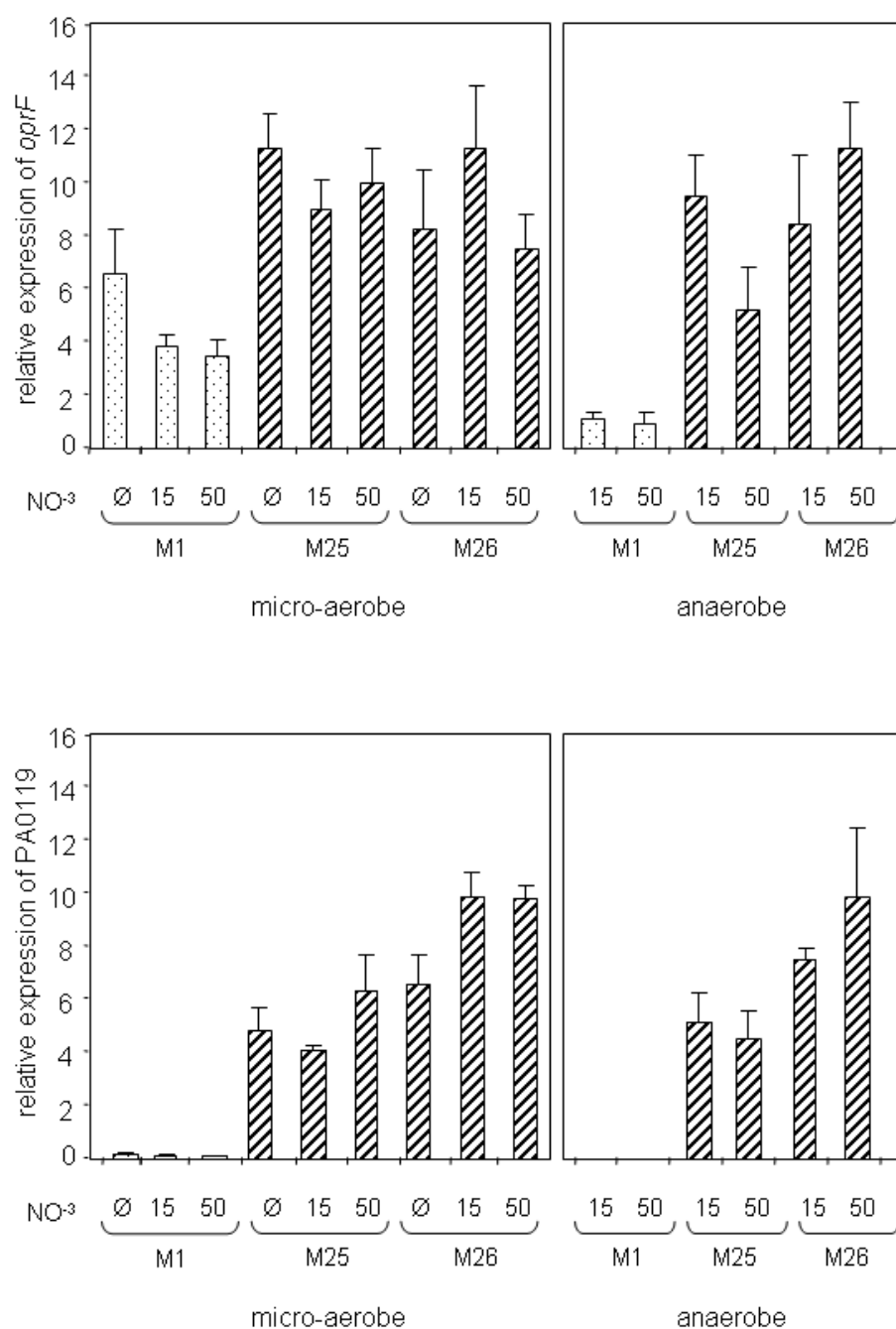


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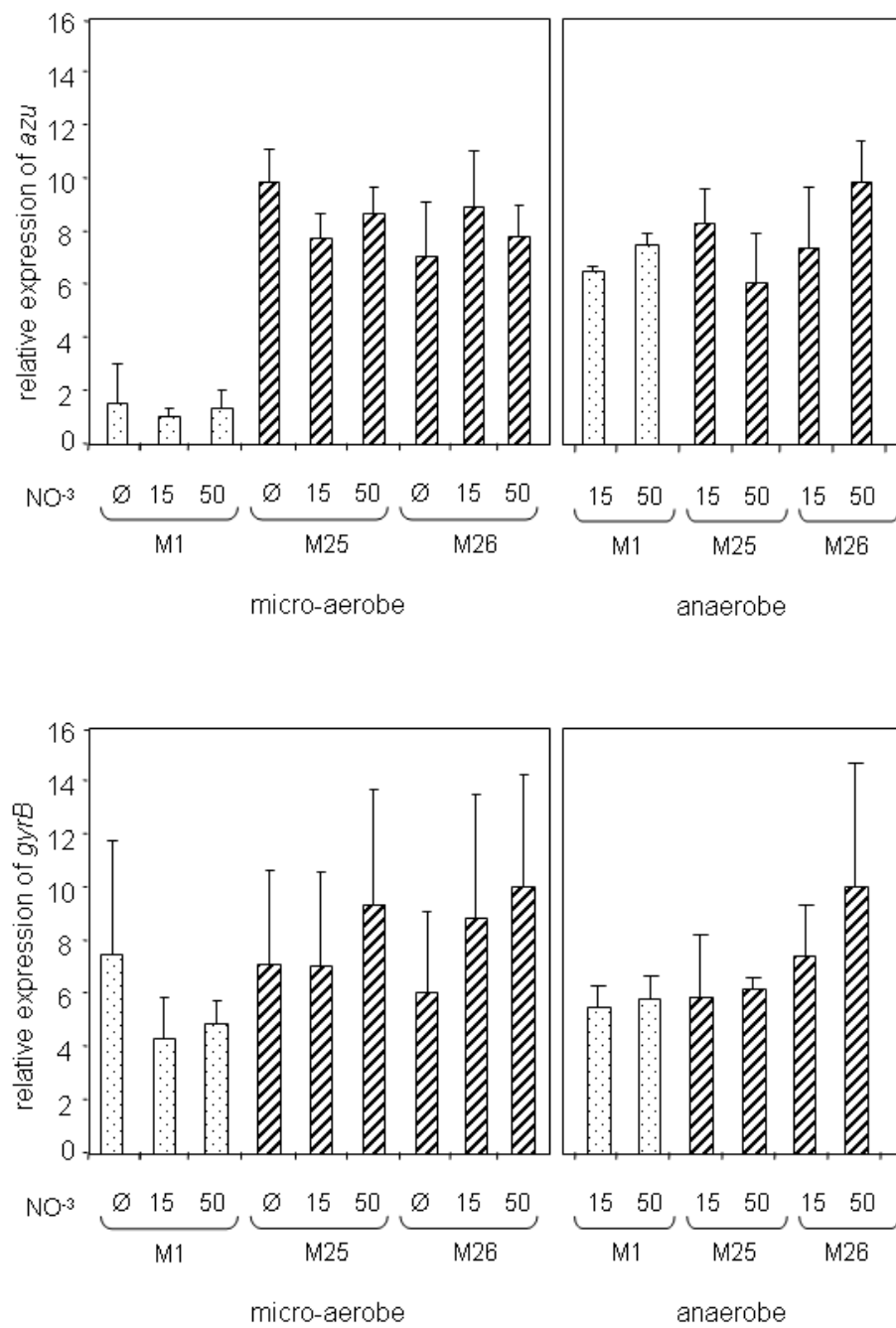


Figure A2:

Mutator M13/M22/M25/M26 vs Non-mutator M1/M9/M11/M23

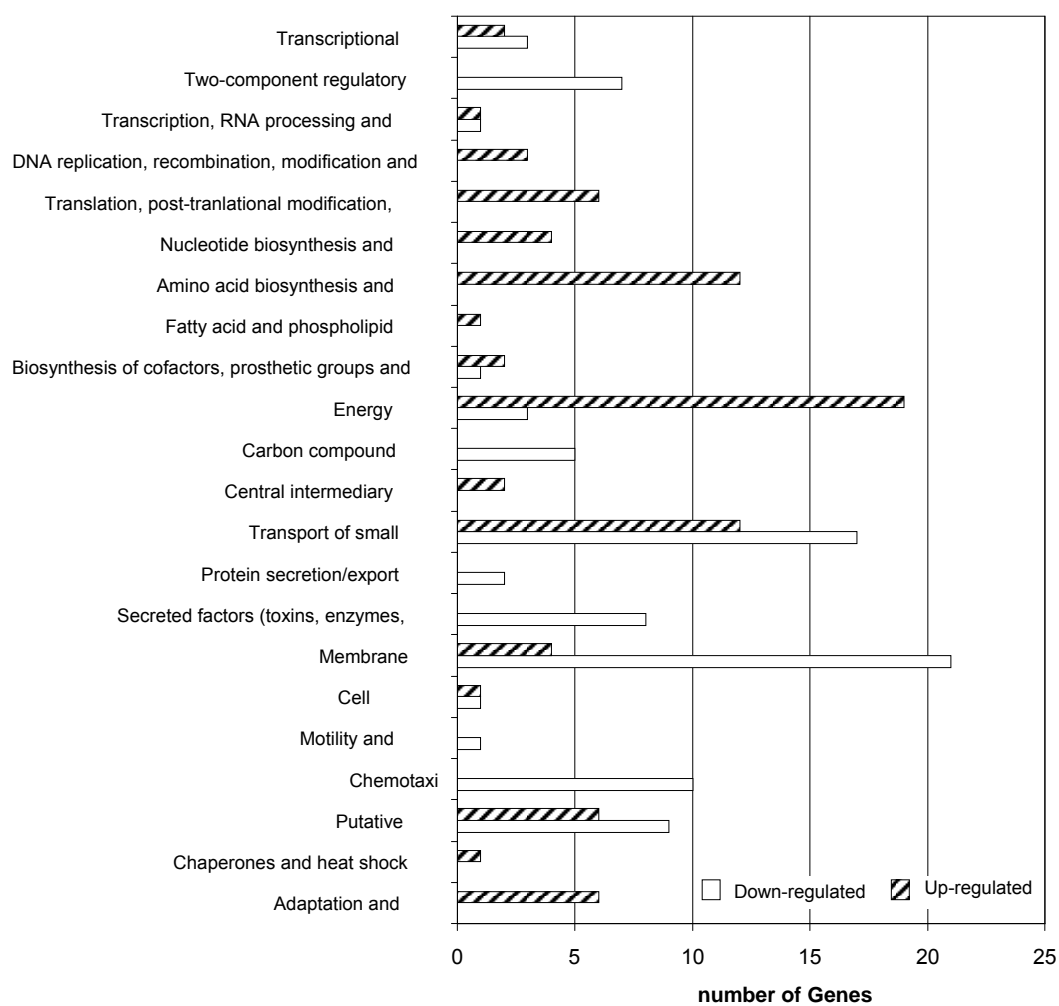


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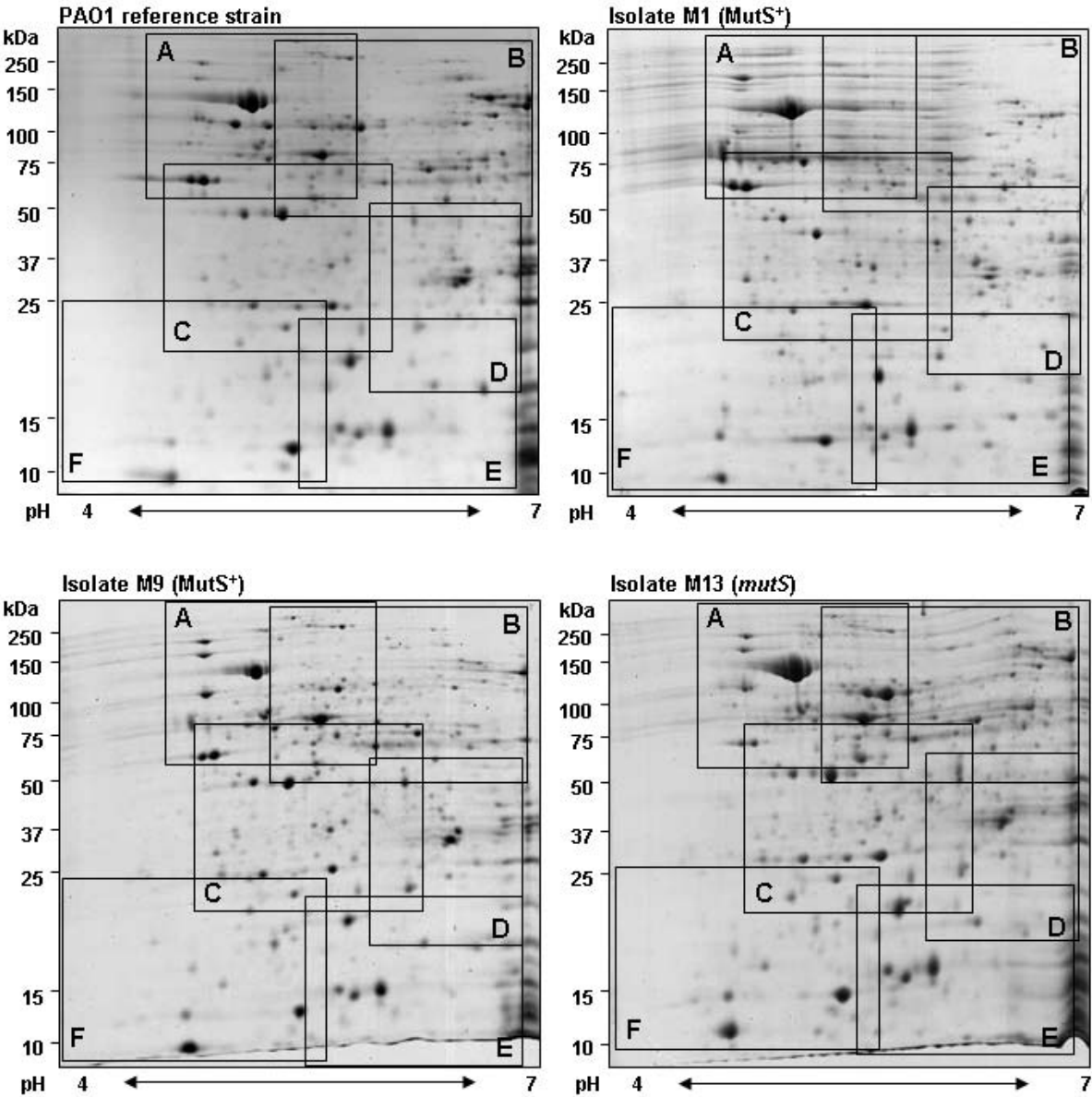


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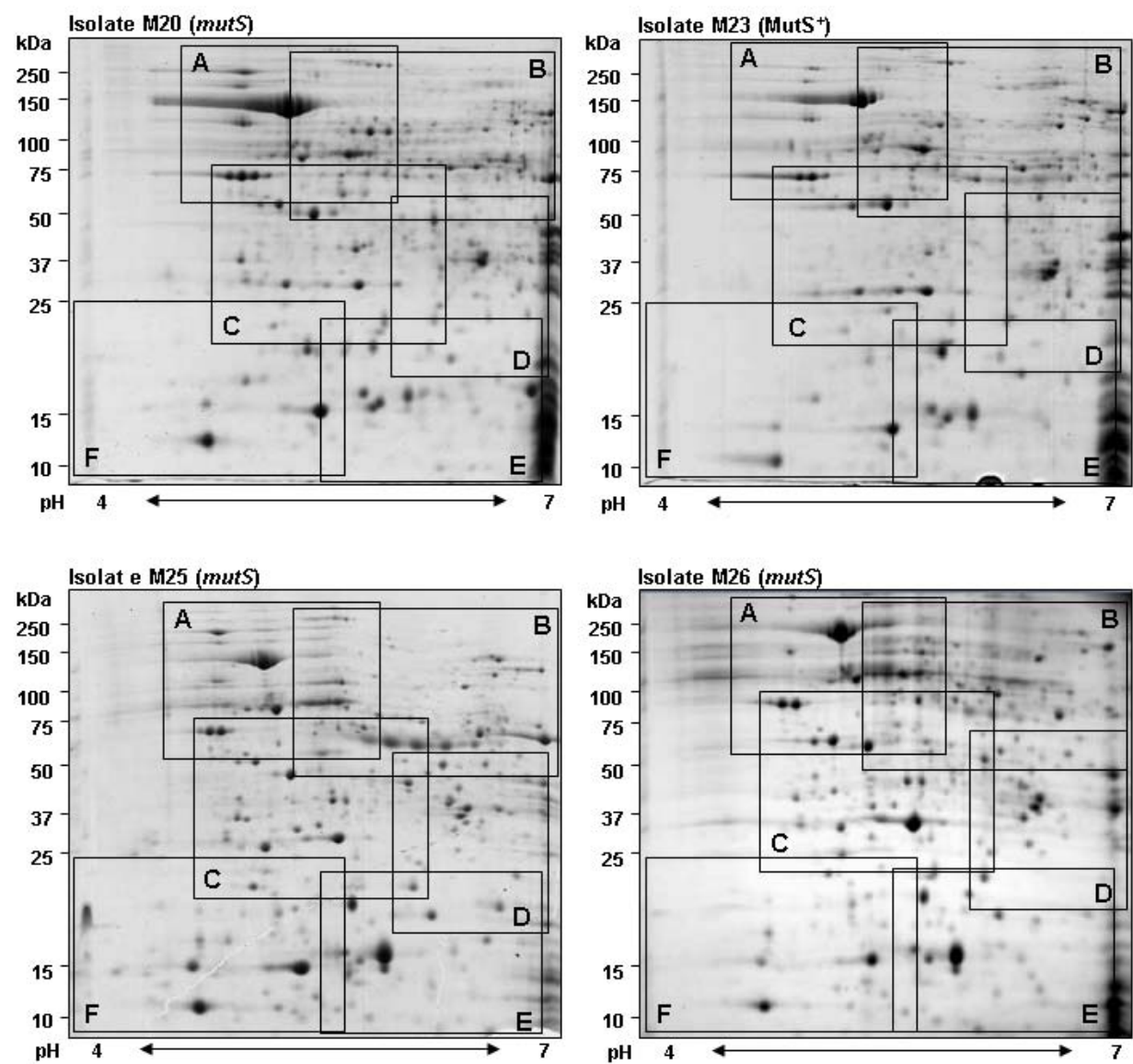


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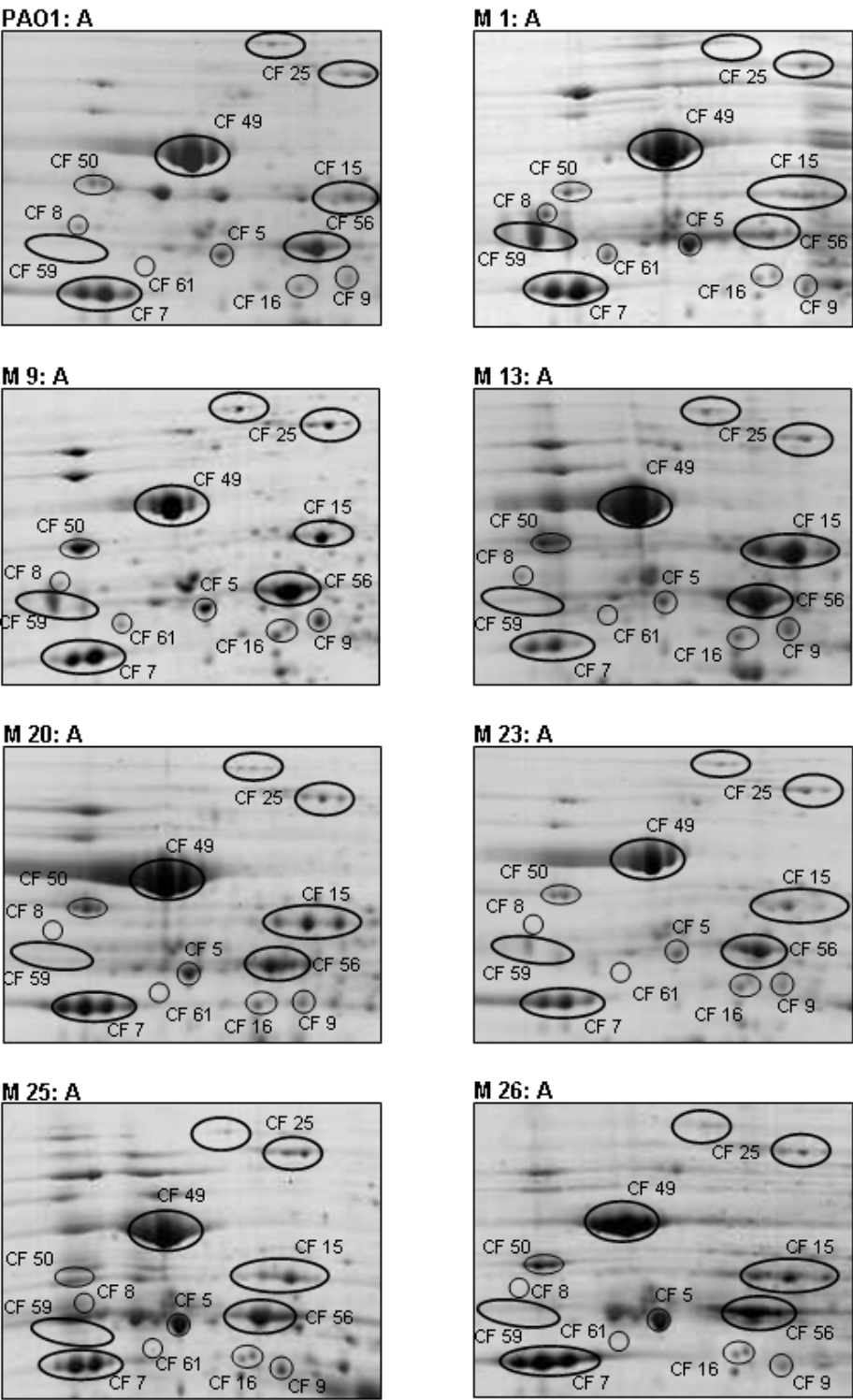
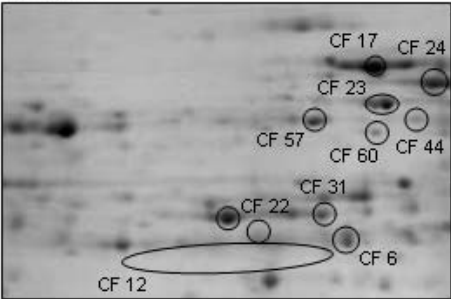


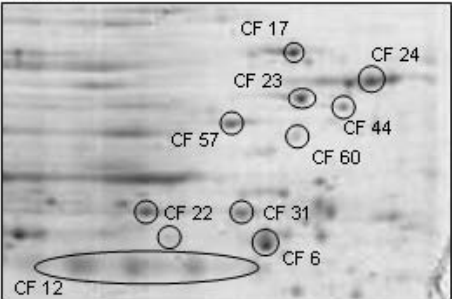
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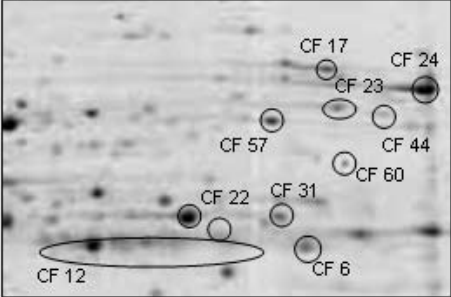
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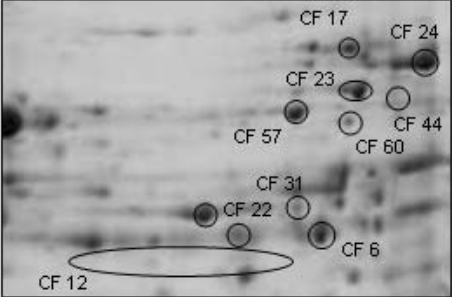
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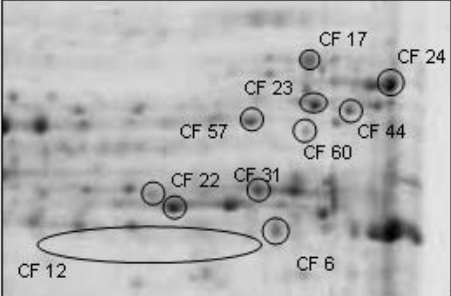
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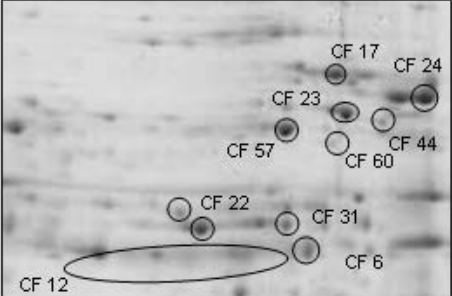
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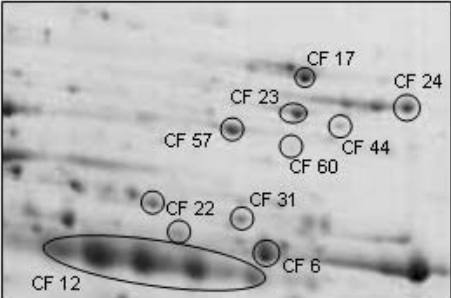
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M 23: B



M 25: B



M 26: B

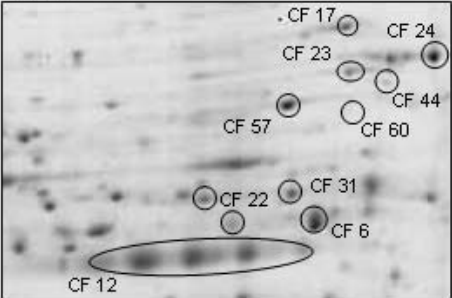
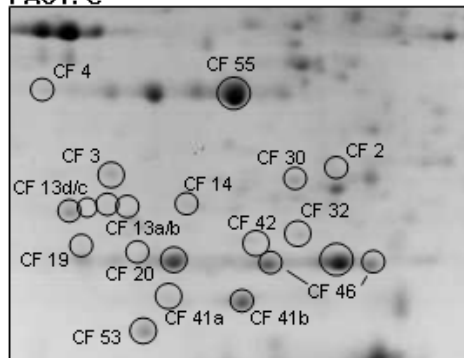


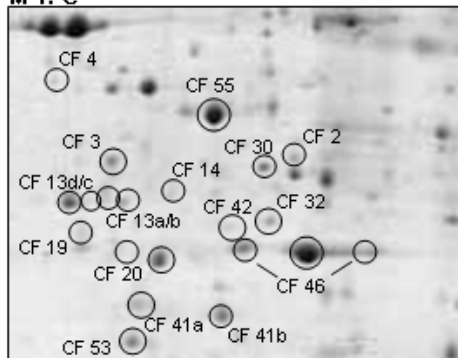
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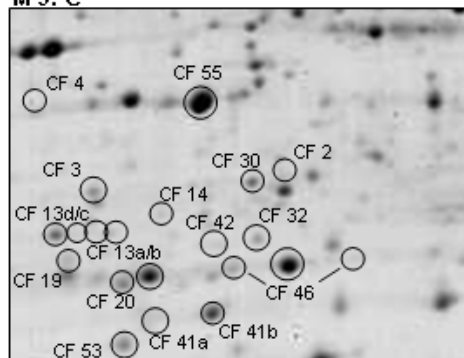
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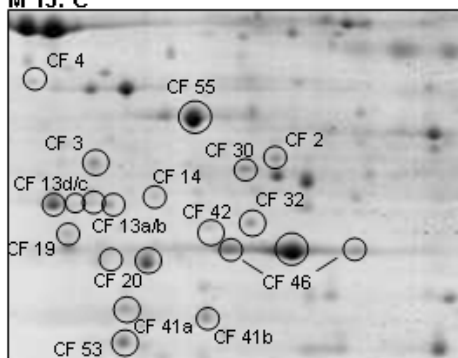
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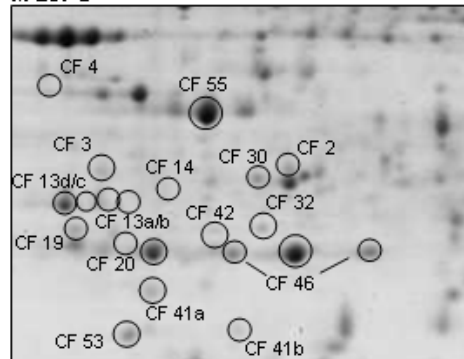
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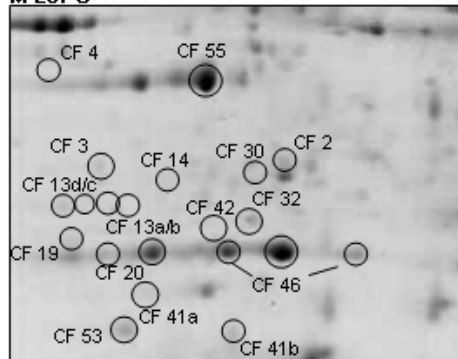
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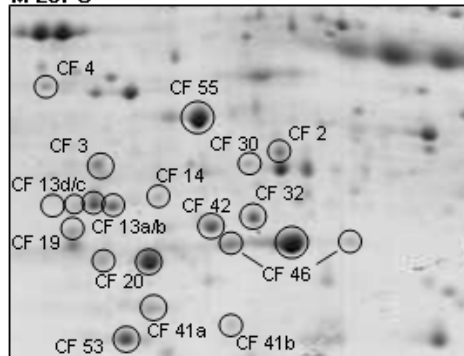
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M 23: C



M 25: C



M 26: C

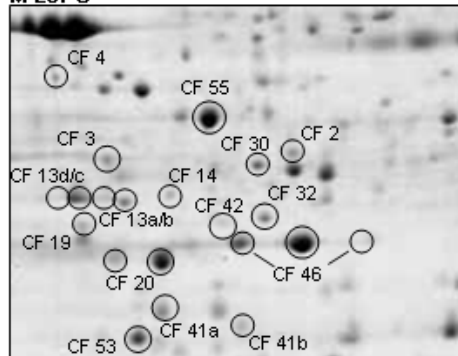


Figure A3 continued:

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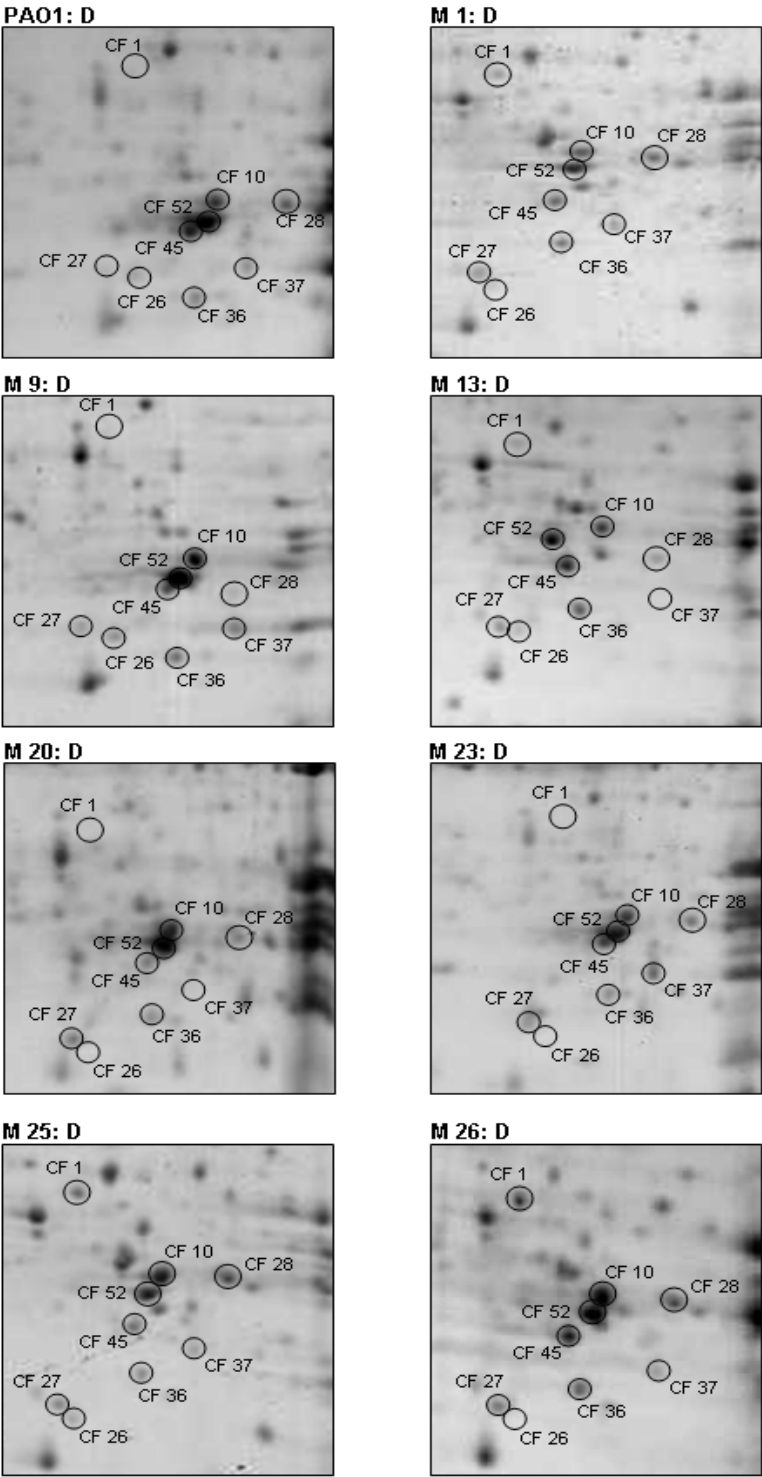
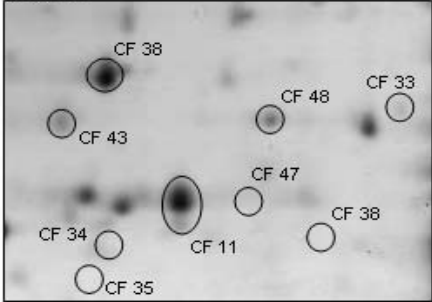


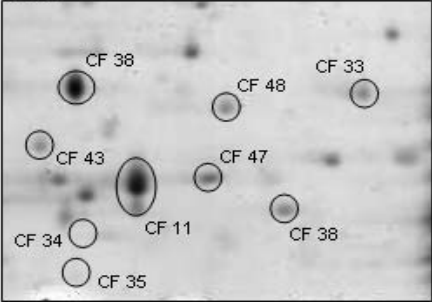
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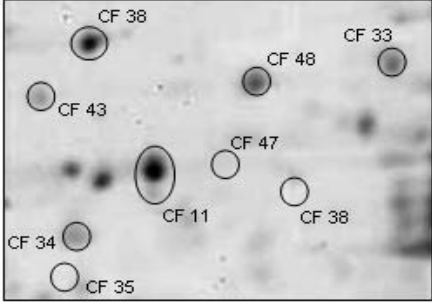
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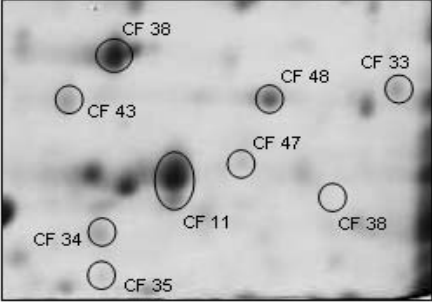
M 1: E



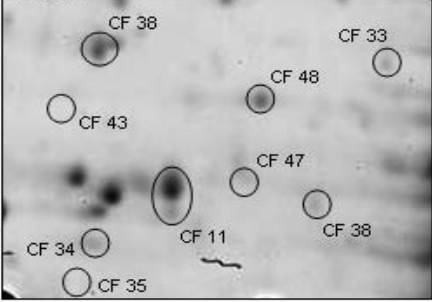
M 9: E



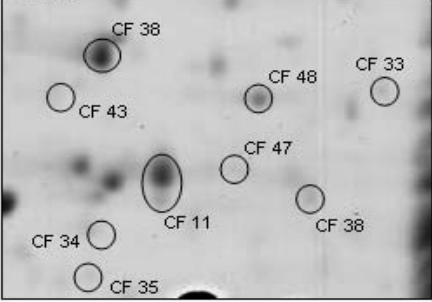
M 13: E



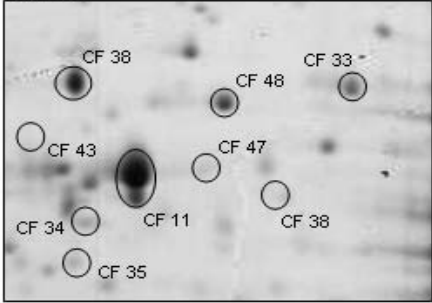
M 20: E



M 23: E



M 25: E



M 26: E

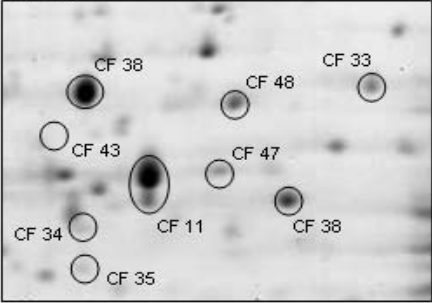


Figure A3 continued:

F

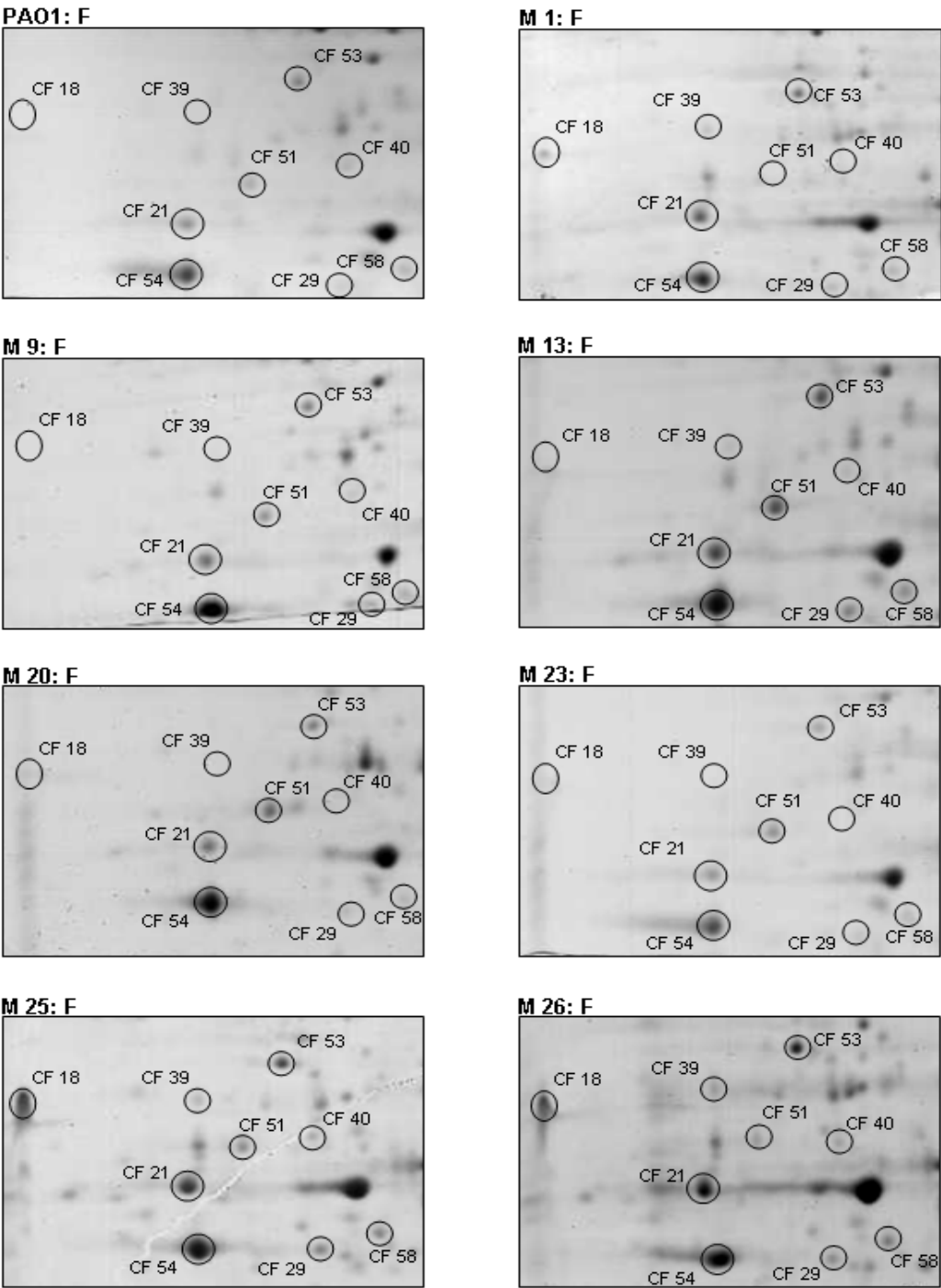


Figure A4: Changes in catabolism of aromatic compounds

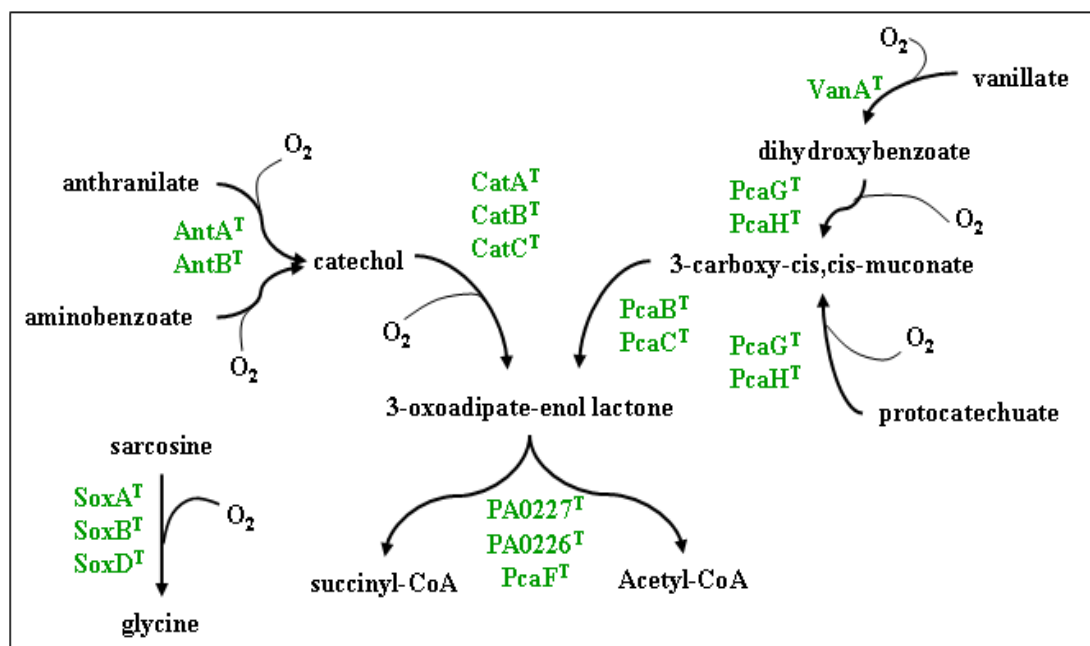
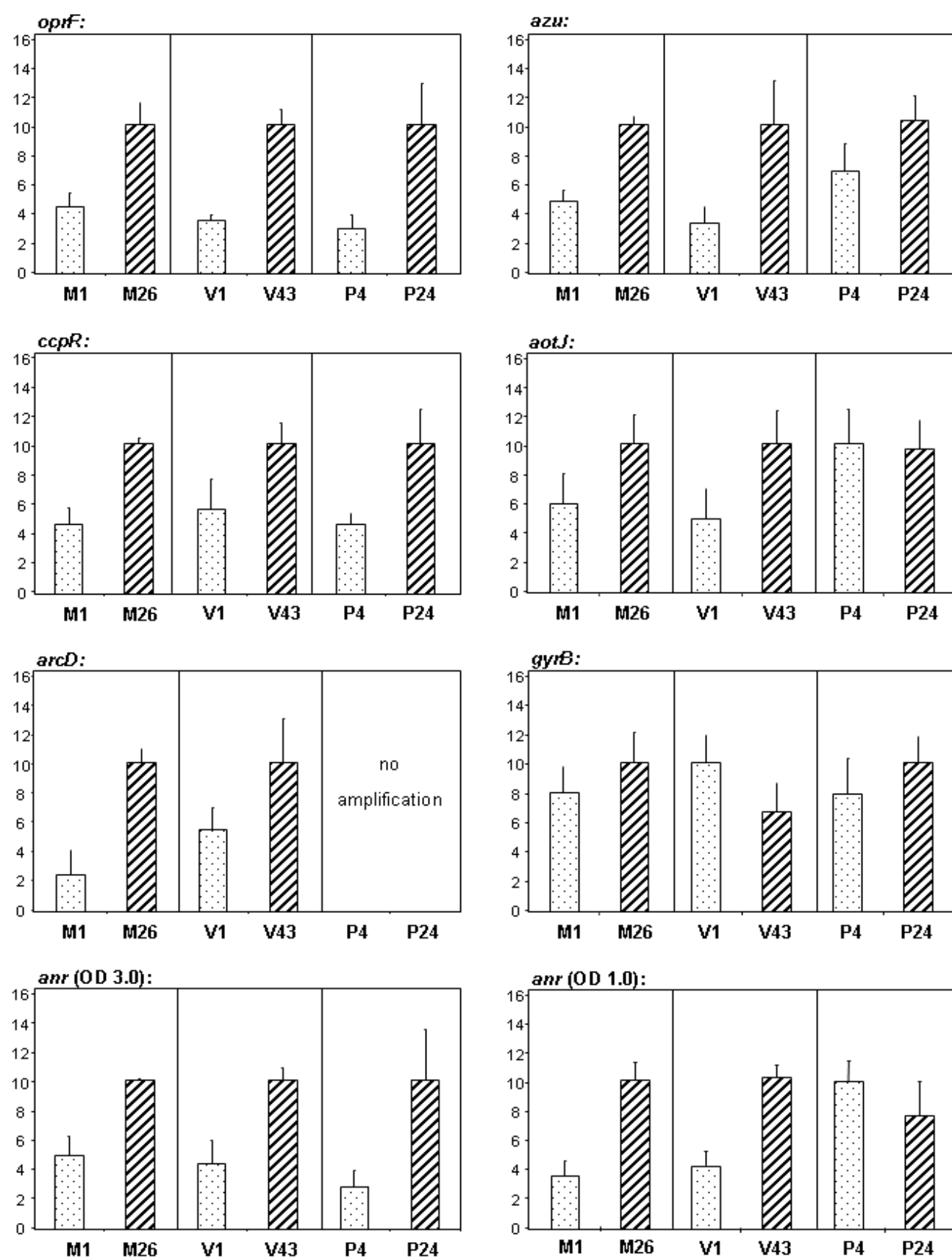


Figure A6:



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Significant Genes List - Table A1

P. aeruginosa mutator (M13/M22/M25/M26) versus non-mutator isolates (M1/M9/M11/M23) of patient M

Input Parameters

Imputation Engine	10-Nearest Neighbor Imputer
Data Type	Two Class, unpaired data
Data in log scale?	FALSCH
Number of Permutations	100
Blocked Permutation?	FALSCH
RNG Seed	1234567
(Delta, Fold Change)	(2,19566, 2,00000)
(Upper Cutoff, Lower Cutoff)	(3,57282, -3,31712)

Computed Quantities

Computed Exchangeability Factor S0	0.068593371
S0 percentile	0
False Significant Number (Median, 90 percentile)	(0,00000, 0,30576)
False Discovery Rate (Median, 90 percentile)	(0,00000, 0,11626)
Pi0Hat	0,30576

122 Positive Significant Genes

Row	Gene Name	Gene ID	Score(d)	Numerator(r)	denominator(s+st)	Fold Change	q-value (%)
822	PA0807_at	PA0807 /DEF=conserved hypothetical protein /FUNC	6.657302564	300.6691667	45.16381279	6,82015	0.089666484
2206	PA2197_at	PA2197 /DEF=conserved hypothetical protein /FUNC	5.702484327	125.3208333	21.97653271	5,17945	0.089666484
2207	PA2198_at	PA2198 /DEF=hypothetical protein /FUNCTION=Hyp	5.099352283	107.5658333	21.09401888	4,75568	0.089666484
2012	PA2002_at	PA2002 /DEF=conserved hypothetical protein /FUNC	3.83681875	171.5116667	44.70152953	4,61858	0.089666484
3464	PA3460_at	PA3460 /DEF=probable acetyltransferase /FUNCTION	5.076464335	330.8975	65.18267009	4,47694	0.089666484
1648	PA1634_kdpB_at	PA1634 /GENE=kdpB /DEF=potassium-transporting	3.73333477	241.9775	64.81537684	4,24675	0.089666484
2758	PA2753_at	PA2753 /DEF=hypothetical protein /FUNCTION=Hyp	3.911337814	357.2075	91.32616946	4,11220	0.089666484
5165	PA5170_arcD_at	PA5170 /GENE=arcD /DEF=arginine/ornithine antipo	5.423951769	1813.003333	334.258749	3,74775	0.089666484
5440	PA5446_i_at	PA5446 /DEF=hypothetical protein /FUNCTION=Hyp	4.527658746	274.0466667	60.52723538	3,44283	0.089666484
1576	PA1562_acnA_at	PA1562 /GENE=acnA /DEF=aconitate hydratase 1 /F	3.961392462	103.9208333	26.23341018	3,40020	0.089666484
2123	PA2114_at	PA2114 /DEF=probable MFS transporter /FUNCTION	4.316612174	381.0008333	88.26385554	3,33221	0.089666484
1647	PA1633_kdpA_at	PA1633 /GENE=kdpA /DEF=potassium-transporting	3.720287905	142.6808333	38.35209451	3,26916	0.089666484
5010	PA5015_aceE_at	PA5015 /GENE=aceE /DEF=pyruvate dehydrogenas	4.450916482	337.8308333	75.90140922	3,26825	0.089666484

1588 PA1574_at	PA1574 /DEF=conserved hypothetical protein /FUNC	3.680026431	142.6975	38.77621606	3,22660	0.089666484
3535 PA3531_bfrB_at	PA3531 /GENE=bfrB /DEF=bacterioferritin /FUNCTION	4.90765059	148.69	30.29759297	3,18504	0.089666484
497 PA0482_glcB_at	PA0482 /GENE=glcB /DEF=malate synthase G /FUNCTION	6.006212125	568.525	94.65616401	3,11236	0.089666484
2208 PA2199_at	PA2199 /DEF=probable dehydrogenase /FUNCTION	5.210193519	83.33833333	15.99524721	3,08480	0.089666484
1594 PA1580_gltA_at	PA1580 /GENE=gltA /DEF=citrate synthase /FUNCTION	8.930365413	912.9708333	102.2321922	3,05005	0.089666484
1585 PA1571_at	PA1571 /DEF=hypothetical protein /FUNCTION=Hyp	4.048528017	433.9933333	107.197809	3,03726	0.089666484
1649 PA1635_kdpC_at	PA1635 /GENE=kdpC /DEF=potassium-transporting	4.001342527	138.4483333	34.60047032	3,00330	0.089666484
3283 PA3278_at	PA3278 /DEF=hypothetical protein /FUNCTION=Hyp	4.464079404	169.5183333	37.97386157	2,95711	0.089666484
3463 PA3459_at	PA3459 /DEF=probable glutamine amidotransferase	4.055843609	208.8908333	51.50367062	2,88876	0.089666484
1215 PA1200_at	PA1200 /DEF=conserved hypothetical protein /FUNCTION	4.317235331	128.0758333	29.66616909	2,87036	0.089666484
2581 PA2575_at	PA2575 /DEF=hypothetical protein /FUNCTION=Hyp	8.340475371	139.4266667	16.71687289	2,82747	0.089666484
1979 PA1969_at	PA1969 /DEF=hypothetical protein /FUNCTION=Hyp	7.847612415	114.8466667	14.63459975	2,80987	0.089666484
977 PA0962_at	PA0962 /DEF=probable dna-binding stress protein /FUNCTION	7.274404101	714.0241667	98.15569176	2,80933	0.089666484
2026 PA2016_at	PA2016 /DEF=probable transcriptional regulator /FUNCTION	4.227354211	729.43	172.5500073	2,76915	0.089666484
5011 PA5016_aceF_at	PA5016 /GENE=aceF /DEF=dihydrolipoamide acetyltransferase	5.056852269	266.4341667	52.68774971	2,76285	0.089666484
4601 PA4605_at	PA4605 /DEF=conserved hypothetical protein /FUNCTION	4.318137647	205.2616667	47.53476694	2,75416	0.089666484
2460 PA2453_at	PA2453 /DEF=hypothetical protein /FUNCTION=Hyp	4.212726197	47.60833333	11.30107467	2,73716	0.089666484
958 PA0943_at	PA0943 /DEF=hypothetical protein /FUNCTION=Hyp	5.564247843	227.6041667	40.90474995	2,73712	0.089666484
2652 PA2646_nuoK_at	PA2646 /GENE=nuoK /DEF=NADH dehydrogenase I	7.35917569	164.75	22.38701819	2,70046	0.089666484
2649 PA2643_nuoH_at	PA2643 /GENE=nuoH /DEF=NADH dehydrogenase I	6.533383041	239.5016667	36.65813946	2,66154	0.089666484
2759 PA2754_at	PA2754 /DEF=conserved hypothetical protein /FUNCTION	3.619534147	266.3891667	73.59763878	2,64479	0.089666484
887 PA0872_phhA_at	PA0872 /GENE=phhA /DEF=phenylalanine-4-hydroxylase	4.248503414	1057.98	249.0241615	2,61408	0.089666484
984 PA0969_tolQ_at	PA0969 /GENE=tolQ /DEF=TolQ protein /FUNCTION	4.411271649	138.2675	31.34413634	2,57211	0.089666484
2653 PA2647_nuoL_at	PA2647 /GENE=nuoL /DEF=NADH dehydrogenase I	5.291844754	88.9675	16.8121901	2,57133	0.089666484
956 PA0941_at	PA0941 /DEF=hypothetical protein /FUNCTION=Hyp	4.268068217	42.12666667	9.870195255	2,53430	0.089666484
1355 PA1340_at	PA1340 /DEF=probable permease of ABC transporter	6.245119175	66.27	10.61148685	2,52289	0.089666484
3817 PA3813_iscU_at	PA3813 /GENE=iscU /DEF=probable iron-binding protein	5.280231381	165.3708333	31.31886113	2,51993	0.089666484
1193 PA1178_oprH_at	PA1178 /GENE=oprH /DEF=outer membrane protein	3.822991026	600.1883333	156.9944395	2,50817	0.089666484
2488 PA2482_at	PA2482 /DEF=probable cytochrome c /FUNCTION=Fe	5.192816633	50.2275	9.672496365	2,49784	0.089666484
1530 PA1516_at	PA1516 /DEF=hypothetical protein /FUNCTION=Hyp	4.083130138	47.36083333	11.59914863	2,49066	0.089666484
5455 PA5461_at	PA5461 /DEF=hypothetical protein /FUNCTION=Hyp	5.779159844	286.6508333	49.60077954	2,46817	0.089666484
2749 PA2744_thrS_at	PA2744 /GENE=thrS /DEF=threonyl-tRNA synthetase	4.699805498	113.9166667	24.23859173	2,45660	0.089666484
2655 PA2649_nuoN_at	PA2649 /GENE=nuoN /DEF=NADH dehydrogenase I	5.990534065	66.21	11.05243694	2,44582	0.089666484
5499 PA5505_at	PA5505 /DEF=probable TonB-dependent receptor /FUNCTION	4.444143608	177.9316667	40.03733505	2,42914	0.089666484
2975 PA2970_rpmF_at	PA2970 /GENE=rpmF /DEF=50S ribosomal protein L	3.846355932	158.3666667	41.17317	2,42757	0.089666484
2651 PA2645_nuoJ_at	PA2645 /GENE=nuoJ /DEF=NADH dehydrogenase I	5.721315218	91.15083333	15.93179712	2,42331	0.089666484

902 PA0887_acsA_at	PA0887 /GENE=acsA /DEF=acetyl-coenzyme A synt	4.626635332	521.7208333	112.7646326	2,42207	0.089666484
3923 PA3919_at	PA3919 /DEF=conserved hypothetical protein /FUNC	4.058548526	136.4425	33.61854592	2,42139	0.089666484
2122 PA2113_at	PA2113 /DEF=probable porin /FUNCTION=Transpor	4.236862411	522.2966667	123.2743988	2,40590	0.089666484
5300 PA5306_at	PA5306 /DEF=conserved hypothetical protein /FUNC	6.306686464	160.6433333	25.47190736	2,39261	0.089666484
2665 PA2659_at	PA2659 /DEF=hypothetical protein /FUNCTION=Hyp	4.324181311	91.67916667	21.20150847	2,38610	0.089666484
920 PA0905_csrA_at	PA0905 /GENE=csrA /DEF=carbon storage regulator	4.119469889	176.0508333	42.73628357	2,38256	0.089666484
3773 PA3769_guaA_at	PA3769 /GENE=guaA /DEF=GMP synthase /FUNCT	4.051151272	304.515	75.16752142	2,38046	0.089666484
2647 PA2641_nuoF_at	PA2641 /GENE=nuoF /DEF=NADH dehydrogenase I	5.861393302	143.4766667	24.47825274	2,37856	0.089666484
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2810 PA2805_at	PA2805 /DEF=hypothetical protein /FUNCTION=Hyp	3.651728452	227.4616667	62.28876809	2,35749	0.089666484
2452 PA2445_gcvP2_at	PA2445 /GENE=gcvP2 /DEF=glycine cleavage syste	3.713070879	237.6616667	64.0067681	2,34290	0.089666484
4263 PA4266_fusA1_at	PA4266 /GENE=fusA1 /DEF=elongation factor G /FU	3.572958315	502.6716667	140.6878061	2,32675	0.089666484
2654 PA2648_nuoM_at	PA2648 /GENE=nuoM /DEF=NADH dehydrogenase	5.103506132	88.55583333	17.35195982	2,30824	0.089666484
2650 PA2644_nuoI_at	PA2644 /GENE=nuoI /DEF=NADH Dehydrogenase I	6.350626908	142.5066667	22.43977937	2,28770	0.089666484
3576 PA3572_at	PA3572 /DEF=hypothetical protein /FUNCTION=Hyp	3.867523127	404.6791667	104.6352286	2,28358	0.089666484
3774 PA3770_guaB_at	PA3770 /GENE=guaB /DEF=inosine-5'-monophosph	3.609645878	162.0316667	44.88852152	2,28089	0.089666484
2645 PA2639_nuoD_at	PA2639 /GENE=nuoD /DEF=NADH dehydrogenase I	4.30530332	101.5666667	23.59105947	2,27659	0.089666484
4069 PA4067_oprG_at	PA4067 /GENE=oprG /DEF=outer membrane protein	4.145600323	642.5283333	154.9904196	2,27624	0.089666484
464 PA0449_at	PA0449 /DEF=hypothetical protein /FUNCTION=Hyp	5.343349312	282.6191667	52.89176323	2,26696	0.089666484
4461 PA4465_at	PA4465 /DEF=conserved hypothetical protein /FUNC	4.844210114	160.9216667	33.21938208	2,26672	0.089666484
3362 PA3357_dsdA_at	PA3357 /GENE=dsdA /DEF=D-serine dehydratase /F	4.110254996	56.02333333	13.63013569	2,25189	0.089666484
4736 PA4740_pnp_at	PA4740 /GENE=pnp /DEF=polyribonucleotide nuclec	4.10265568	172.9541667	42.1566371	2,24841	0.089666484
5333 PA5339_at	PA5339 /DEF=conserved hypothetical protein /FUNC	4.935135083	452.6641667	91.72275105	2,24446	0.089666484
1547 PA1533_at	PA1533 /DEF=conserved hypothetical protein /FUNC	6.839061568	310.2533333	45.36489842	2,24310	0.089666484
2629 PA2623_icd_at	PA2623 /GENE=icd /DEF=isocitrate dehydrogenase /	7.052778324	784.9641667	111.2985735	2,24226	0.089666484
4002 PA3999_dacC_at	PA3999 /GENE=dacC /DEF=D-ala-D-ala-carboxypep	5.766934633	298.3616667	51.73661323	2,23800	0.089666484
2538 PA2532_tpx_at	PA2532 /GENE=tpx /DEF=thiol peroxidase /FUNCTI	4.394486387	219.8241667	50.02272104	2,23392	0.089666484
2119 PA2110_at	PA2110 /DEF=hypothetical protein /FUNCTION=Hyp	3.771071024	282.9591667	75.03416533	2,23343	0.089666484
5013 PA5018_msrA_at	PA5018 /GENE=msrA /DEF=peptide methionine sulf	5.678433582	182.1908333	32.08469919	2,23001	0.089666484
4092 PA4090_at	PA4090 /DEF=hypothetical protein /FUNCTION=Hyp	3.882907068	153.5916667	39.55584411	2,22999	0.089666484
1817 PA1803_lon_at	PA1803 /GENE=lon /DEF=Lon protease /FUNCTION	6.192499371	292.81	47.28462329	2,22421	0.089666484
4691 PA4695_ilvH_at	PA4695 /GENE=ilvH /DEF=acetolactate synthase iso	5.3370787	231.4541667	43.36720136	2,22303	0.089666484
1528 PA1514_at	PA1514 /DEF=conserved hypothetical protein /FUNC	4.933881887	29.5125	5.9815984	2,22032	0.089666484
983 PA0968_at	PA0968 /DEF=conserved hypothetical protein /FUNC	4.229450304	73.5525	17.39055781	2,22015	0.089666484
4234 PA4237_rplQ_at	PA4237 /GENE=rplQ /DEF=50S ribosomal protein L1	3.672013743	422.53	115.0676521	2,20646	0.089666484
1028 PA1013_purC_at	PA1013 /GENE=purC /DEF=phosphoribosylaminoimi	5.426971068	105.2158333	19.38757956	2,20231	0.089666484

916	PA0901_aruE_at	PA0901 /GENE=aruE /DEF=succinylglutamate desuc	3.972343858	99.84083333	25.1339856	2,18565	0.089666484
3619	PA3615_at	PA3615 /DEF=hypothetical protein /FUNCTION=Hyp	4.463597552	101.3716667	22.71075416	2,18000	0.089666484
2648	PA2642_nuoG_at	PA2642 /GENE=nuoG /DEF=NADH dehydrogenase 	5.132917442	202.9516667	39.53924234	2,16731	0.089666484
2644	PA2638_nuoB_at	PA2638 /GENE=nuoB /DEF=NADH dehydrogenase 	5.443717414	96.96083333	17.81151113	2,16318	0.089666484
4001	PA3998_at	PA3998 /DEF=conserved hypothetical protein /FUNC	6.649252316	129.9908333	19.54969178	2,15459	0.089666484
987	PA0972_tolB_at	PA0972 /GENE=tolB /DEF=TolB protein /FUNCTION	5.942173523	338.0141667	56.8839273	2,12354	0.089666484
1806	PA1792_at	PA1792 /DEF=conserved hypothetical protein /FUNC	4.274795079	85.53416667	20.00895133	2,10711	0.089666484
1809	PA1795_cysS_at	PA1795 /GENE=cysS /DEF=cysteinyI-tRNA syntheta	4.62219781	68.93666667	14.91426146	2,10213	0.089666484
4200	PA4198_at	PA4198 /DEF=probable AMP-binding enzyme /FUNC	3.967952882	182.5791667	46.01344122	2,09668	0.089666484
330	PA0315_at	PA0315 /DEF=hypothetical protein /FUNCTION=Hyp	5.903458419	260.8891667	44.19259833	2,09235	0.089666484
4229	PA4232_ssb_at	PA4232 /GENE=ssb /DEF=single-stranded DNA-binc	3.743920967	180.3283333	48.16563569	2,08627	0.089666484
4531	PA4535_at	PA4535 /DEF=hypothetical protein /FUNCTION=Hyp	6.286731978	73.03333333	11.61705853	2,07687	0.089666484
3835	PA3831_pepA_at	PA3831 /GENE=pepA /DEF=leucine aminopeptidase	4.600910559	82.785	17.99317742	2,07199	0.089666484
1085	PA1070_braG_at	PA1070 /GENE=braG /DEF=branched-chain amino a	4.239757245	180.7733333	42.63766129	2,07063	0.089666484
1808	PA1794_glnS_at	PA1794 /GENE=glnS /DEF=glutaminyI-tRNA synthet	3.737190311	92.33416667	24.70684097	2,06976	0.089666484
2610	PA2604_at	PA2604 /DEF=conserved hypothetical protein /FUNC	4.702228646	280.87	59.73125111	2,06969	0.089666484
19	PA0004_gyrB_at	PA0004 /GENE=gyrB /DEF=DNA gyrase subunit B /F	4.357513874	117.0066667	26.85170261	2,05863	0.089666484
281	PA0266_gabT_at	PA0266 /GENE=gabT /DEF=4-aminobutyrate aminot	3.577403308	333.3	93.16813659	2,05770	0.089666484
4178	PA4176_ppiC2_at	PA4176 /GENE=ppiC2 /DEF=peptidyl-prolyl cis-trans	4.346099441	94.3675	21.71314791	2,05603	0.089666484
3836	PA3832_holC_at	PA3832 /GENE=holC /DEF=DNA polymerase III, chi	5.600223252	29.18416667	5.21125058	2,04672	0.089666484
609	PA0594_surA_at	PA0594 /GENE=surA /DEF=peptidyl-prolyl cis-trans i	4.846056222	102.58	21.167728	2,04335	0.089666484
3019	PA3014_faoA_at	PA3014 /GENE=faoA /DEF=fatty-acid oxidation com	5.478017092	117.8566667	21.51447589	2,03794	0.089666484
1354	PA1339_at	PA1339 /DEF=probable ATP-binding component of A	5.35594045	168.0133333	31.36952976	2,03300	0.089666484
2801	PA2796_tal_at	PA2796 /GENE=tal /DEF=transaldolase /FUNCTION:	5.310488	106.405	20.03676498	2,03202	0.089666484
4534	PA4538_ndh_at	PA4538 /GENE=ndh /DEF=NADH dehydrogenase /F	7.344977219	74.79583333	10.18326281	2,03177	0.089666484
2746	PA2741_rplT_at	PA2741 /GENE=rplT /DEF=50S ribosomal protein L2	4.163686109	382.235	91.80206912	2,03097	0.089666484
4752	PA4756_carB_at	PA4756 /GENE=carB /DEF=carbamoylphosphate syr	3.633175601	133.0366667	36.61718598	2,02713	0.089666484
1560	PA1546_hemN_at	PA1546 /GENE=hemN /DEF=oxygen-independent cc	3.784697827	81.30916667	21.48366141	2,02543	0.089666484
4459	PA4463_at	PA4463 /DEF=conserved hypothetical protein /FUNC	4.357186163	1187.78	272.6025365	2,02386	0.089666484
1611	PA1597_at	PA1597 /DEF=hypothetical protein /FUNCTION=Hyp	3.979264162	25.35833333	6.37261873	2,01824	0.089666484
1429	PA1414_at	PA1414 /DEF=hypothetical protein /FUNCTION=Hyp	3.688000578	1647.236667	446.6476162	2,01228	0.089666484
3300	PA3295_at	PA3295 /DEF=probable HIT family protein /FUNCTIC	3.896365234	43.5175	11.1687425	2,00828	0.089666484
1352	PA1337_ansB_at	PA1337 /GENE=ansB /DEF=glutaminase-asparagina	5.601324059	225.7033333	40.29463944	2,00778	0.089666484
3985	PA3981_at	PA3981 /DEF=conserved hypothetical protein /FUNC	3.572820291	112.7791667	31.56586604	2,00748	0.089666484
1822	PA1808_at	PA1808 /DEF=probable permease of ABC transporte	5.995062204	36.35	6.063323243	2,00667	0.089666484
2714	PA2709_cysK_at	PA2709 /GENE=cysK /DEF=cysteine synthase A /FU	6.271941878	240.4875	38.34338785	2,00613	0.089666484

4602 PA4606_at

[PA4606 /DEF=conserved hypothetical protein /FUNC](#)

7.076967392

193.6758333

27.36706595

2,00502

0.089666484

138 Negative Significant Genes

Row	Gene Name	Gene ID	Score(d)	Numerator(r)	denominator(s+s)	Fold Change	q-value (%)
4227	PA4230_pchB_at	PA4230 /GENE=pchB /DEF=salicylate biosynthesis p	-5.972787847	-503.345	84.27304182	0,14801	0.089666484
3530	PA3526_at	PA3526 /DEF=probable outer membrane protein /FU	-5.2889162	-176.1733333	33.30991203	0,20066	0.089666484
4221	PA4224_at	PA4224 /DEF=hypothetical protein /FUNCTION=Hyp	-5.833476694	-672.475	115.2785955	0,21286	0.089666484
4225	PA4228_pchD_at	PA4228 /GENE=pchD /DEF=pyochelin biosynthesis p	-5.164997415	-345.5775	66.90758431	0,21587	0.089666484
4322	PA4326_at	PA4326 /DEF=hypothetical protein /FUNCTION=Hyp	-4.182059251	-168.6941667	40.33758408	0,22060	0.089666484
4217	PA4220_i_at	PA4220 /DEF=hypothetical protein /FUNCTION=Hyp	-4.139824129	-212.3233333	51.28800807	0,23951	0.089666484
4223	PA4226_pchE_at	PA4226 /GENE=pchE /DEF=dihydroaeruginic acid s	-4.797420123	-279.29	58.21670666	0,24153	0.089666484
4226	PA4229_pchC_at	PA4229 /GENE=pchC /DEF=pyochelin biosynthetic p	-5.001425441	-237.1466667	47.41581564	0,24364	0.089666484
4228	PA4231_pchA_at	PA4231 /GENE=pchA /DEF=salicylate biosynthesis i	-5.556154425	-249.6183333	44.92645709	0,24962	0.089666484
2300	PA2292_at	PA2292 /DEF=hypothetical protein /FUNCTION=Hyp	-3.597264404	-57.73666667	16.05015928	0,26828	0.089666484
4222	PA4225_pchF_at	PA4225 /GENE=pchF /DEF=pyochelin synthetase /F	-3.406661401	-99.4625	29.1964737	0,27749	0.089666484
4195	PA4193_at	PA4193 /DEF=probable permease of ABC transporte	-4.716768645	-47.04916667	9.974872674	0,28254	0.089666484
193	PA0178_at	PA0178 /DEF=probable two-component sensor /FUN	-4.817504762	-104.86	21.76645487	0,28636	0.089666484
3908	PA3904_i_at	PA3904 /DEF=hypothetical protein /FUNCTION=Hyp	-5.084785975	-42.93166667	8.443161006	0,28956	0.089666484
4818	PA4823_at	PA4823 /DEF=hypothetical protein /FUNCTION=Hyp	-4.389991891	-45.21666667	10.29994309	0,30065	0.089666484
4215	PA4218_at	PA4218 /DEF=probable transporter /FUNCTION=Me	-5.012704406	-203.3208333	40.56110572	0,30473	0.089666484
4218	PA4221_fptA_at	PA4221 /GENE=fptA /DEF=Fe(III)-pyochelin receptor	-4.299805902	-387.3016667	90.0742209	0,30782	0.089666484
2931	PA2926_hisP_at	PA2926 /GENE=hisP /DEF=histidine transport proteir	-4.434649024	-42.86583333	9.666116328	0,31424	0.089666484
791	PA0776_at	PA0776 /DEF=hypothetical protein /FUNCTION=Hyp	-3.5540592	-48.0725	13.52608308	0,31677	0.089666484
3728	PA3724_lasB_at	PA3724 /GENE=lasB /DEF=elastase LasB /FUNCTIC	-3.566755612	-62.5625	17.54045043	0,31759	0.089666484
2927	PA2922_at	PA2922 /DEF=probable hydrolase /FUNCTION=Put	-4.135447636	-62.28666667	15.06165043	0,31940	0.089666484
4856	PA4861_at	PA4861 /DEF=probable ATP-binding component of A	-3.700875427	-55.63583333	15.03315484	0,32067	0.089666484
4839	PA4844_at	PA4844 /DEF=probable chemotaxis transducer /FUN	-4.076947393	-60.0725	14.73467627	0,33391	0.089666484
4219	PA4222_at	PA4222 /DEF=probable ATP-binding component of A	-5.633551137	-135.5225	24.05631842	0,33428	0.089666484
4780	PA4784_at	PA4784 /DEF=probable transcriptional regulator /FU	-4.59809799	-97.79	21.26748934	0,33585	0.089666484
4829	PA4834_at	PA4834 /DEF=hypothetical protein /FUNCTION=Hyp	-4.313567511	-38.55666667	8.938463712	0,34467	0.089666484
191	PA0176_at	PA0176 /DEF=probable chemotaxis transducer /FUN	-4.362821965	-166.8766667	38.2497081	0,34577	0.089666484
230	PA0215_at	PA0215 /DEF=probable transporter /FUNCTION=Me	-4.565765815	-55.15083333	12.07920764	0,35302	0.089666484
1715	PA1701_at	PA1701 /DEF=conserved hypothetical protein in type	-4.112265415	-59.81666667	14.54591585	0,35531	0.089666484
3312	PA3307_r_at	PA3307 /DEF=hypothetical protein /FUNCTION=Hyp	-3.7940644	-161.7141667	42.62293667	0,35780	0.089666484
4838	PA4843_at	PA4843 /DEF=probable two-component response reg	-4.557180148	-92.06166667	20.20145434	0,36046	0.089666484
399	PA0384_at	PA0384 /DEF=hypothetical protein /FUNCTION=Hyp	-4.08762717	-76.51	18.71746048	0,36118	0.089666484

4924 PA4929_at	PA4929 /DEF=hypothetical protein /FUNCTION=Hyp	-4.100286481	-45.08416667	10.99536993	0,36329	0.089666484
4893 PA4898_at	PA4898 /DEF=probable porin /FUNCTION=Membran	-4.004247042	-57.03916667	14.24466724	0,36564	0.089666484
224 PA0209_at	PA0209 /DEF=conserved hypothetical protein /FUNC	-4.98650253	-62.56	12.54586749	0,36735	0.089666484
4313 PA4317_at	PA4317 /DEF=hypothetical protein /FUNCTION=Hyp	-4.906628571	-102.8991667	20.97146038	0,36744	0.089666484
3744 PA3740_at	PA3740 /DEF=hypothetical protein /FUNCTION=Hyp	-5.681387873	-40.7125	7.165942708	0,37208	0.089666484
4920 PA4925_at	PA4925 /DEF=conserved hypothetical protein /FUNC	-3.514540241	-40.1125	11.41329939	0,37626	0.089666484
4306 PA4310_pctB_at	PA4310 /GENE=pctB /DEF=chemotactic transducer I	-5.250429035	-69.57416667	13.25113933	0,37692	0.089666484
2313 PA2305_at	PA2305 /DEF=probable non-ribosomal peptide synth	-3.603909122	-41.04333333	11.38855946	0,37907	0.089666484
4040 PA4038_at	PA4038 /DEF=hypothetical protein /FUNCTION=Hyp	-4.100567524	-24.77916667	6.04286273	0,37914	0.089666484
4220 PA4223_at	PA4223 /DEF=probable ATP-binding component of A	-4.74265824	-137.4966667	28.99147687	0,38172	0.089666484
4772 PA4776_at	PA4776 /DEF=probable two-component response reg	-5.014924314	-92.5875	18.46239229	0,38189	0.089666484
1706 PA1692_at	PA1692 /DEF=probable translocation protein in type I	-3.423461391	-87.28916667	25.49734222	0,38302	0.089666484
4854 PA4859_at	PA4859 /DEF=probable permease of ABC transporte	-4.493083985	-91.60333333	20.38762988	0,38427	0.089666484
2872 PA2867_at	PA2867 /DEF=probable chemotaxis transducer /FUN	-4.310266598	-181.9883333	42.22205963	0,38482	0.089666484
2084 PA2075_at	PA2075 /DEF=hypothetical protein /FUNCTION=Hyp	-3.560227259	-39.185	11.00631986	0,38746	0.089666484
3433 PA3428_at	PA3428 /DEF=hypothetical protein /FUNCTION=Hyp	-5.110698457	-38.94333333	7.619963037	0,38940	0.089666484
3223 PA3218_at	PA3218 /DEF=hypothetical protein /FUNCTION=Hyp	-3.873915416	-35.83166667	9.249470579	0,38941	0.089666484
2085 PA2076_at	PA2076 /DEF=probable transcriptional regulator /FUN	-3.918870559	-51.07916667	13.0341551	0,39057	0.089666484
4587 PA4591_at	PA4591 /DEF=hypothetical protein /FUNCTION=Hyp	-3.907928377	-60.9375	15.59330011	0,39077	0.089666484
203 PA0188_at	PA0188 /DEF=hypothetical protein /FUNCTION=Hyp	-3.795202108	-60.93416667	16.05557884	0,39154	0.089666484
4812 PA4817_at	PA4817 /DEF=hypothetical protein /FUNCTION=Hyp	-4.293813972	-87.65416667	20.41405781	0,39384	0.089666484
3910 PA3906_at	PA3906 /DEF=hypothetical protein /FUNCTION=Hyp	-4.979677006	-38.71916667	7.775437367	0,39716	0.089666484
401 PA0386_at	PA0386 /DEF=probable oxidase /FUNCTION=Putativ	-4.801392091	-45.24083333	9.422440925	0,39734	0.089666484
225 PA0210_mdcC_at	PA0210 /GENE=mdcC /DEF=malonate decarboxylas	-4.075093424	-31.68	7.7740549	0,39879	0.089666484
2343 PA2336_at	PA2336 /DEF=hypothetical protein /FUNCTION=Hyp	-3.737011931	-40.17916667	10.75168274	0,39973	0.089666484
5173 PA5178_at	PA5178 /DEF=conserved hypothetical protein /FUNC	-4.442084385	-1226.145	276.0292002	0,40954	0.089666484
2887 PA2882_at	PA2882 /DEF=probable two-component sensor /FUN	-4.009023924	-40.94416667	10.21300133	0,40975	0.089666484
4778 PA4782_at	PA4782 /DEF=hypothetical protein /FUNCTION=Hyp	-5.480160318	-169.9616667	31.01399536	0,41103	0.089666484
2291 PA2282_at	PA2282 /DEF=hypothetical protein /FUNCTION=Hyp	-3.540137891	-39.55916667	11.17447057	0,41134	0.089666484
190 PA0175_at	PA0175 /DEF=probable chemotaxis protein methyltra	-4.404058083	-41.12166667	9.337221692	0,41263	0.089666484
5096 PA5101_at	PA5101 /DEF=hypothetical protein /FUNCTION=Hyp	-4.58949689	-112.7858333	24.57477062	0,41732	0.089666484
4216 PA4219_at	PA4219 /DEF=hypothetical protein /FUNCTION=Hyp	-5.673194236	-86.76833333	15.29444079	0,41765	0.089666484
5462 PA5468_at	PA5468 /DEF=probable citrate transporter /FUNCTIC	-4.873063234	-29.53333333	6.060527417	0,41870	0.089666484
2921 PA2916_at	PA2916 /DEF=hypothetical protein /FUNCTION=Hyp	-3.942070798	-54.225	13.75546072	0,41899	0.089666484
256 PA0241_at	PA0241 /DEF=probable MFS transporter /FUNCTION	-4.450487827	-60.97916667	13.70168149	0,41974	0.089666484
4629 PA4633_at	PA4633 /DEF=probable chemotaxis transducer /FUN	-3.726174271	-147.9416667	39.70336755	0,43009	0.089666484

2305	PA2297_at	PA2297 /DEF=probable ferredoxin /FUNCTION=Ene	-3.554152534	-62.11833333	17.47767794	0,43415	0.089666484
3878	PA3874_narH_at	PA3874 /GENE=narH /DEF=respiratory nitrate reduci	-4.080567816	-32.055	7.85552439	0,44131	0.089666484
4976	PA4981_at	PA4981 /DEF=probable amino acid permease /FUNC	-4.170873812	-34.20666667	8.201319006	0,44420	0.089666484
2340	PA2333_at	PA2333 /DEF=probable sulfatase /FUNCTION=Putat	-3.787675337	-33.85916667	8.939300139	0,44450	0.089666484
4106	PA4104_at	PA4104 /DEF=conserved hypothetical protein /FUNC	-4.138072426	-40.64166667	9.821400516	0,44496	0.089666484
4851	PA4856_at	PA4856 /DEF=probable sensor/response regulator h	-4.686790161	-174.4016667	37.21132388	0,44732	0.089666484
5026	PA5031_at	PA5031 /DEF=probable short chain dehydrogenase /	-4.086724027	-28.58583333	6.994803941	0,44830	0.089666484
4821	PA4826_at	PA4826 /DEF=hypothetical protein /FUNCTION=Hyp	-3.740735074	-26.88166667	7.186199006	0,45008	0.089666484
4378	PA4382_at	PA4382 /DEF=hypothetical protein /FUNCTION=Hyp	-3.681260934	-30.51083333	8.288147427	0,45019	0.089666484
4833	PA4838_at	PA4838 /DEF=hypothetical protein /FUNCTION=Hyp	-4.074393735	-28.3875	6.967294239	0,45031	0.089666484
2873	PA2868_i_at	PA2868 /DEF=hypothetical protein /FUNCTION=Hyp	-4.925113396	-36.58916667	7.429101367	0,45195	0.089666484
3224	PA3219_at	PA3219 /DEF=hypothetical protein /FUNCTION=Hyp	-4.299232259	-52.9475	12.31557097	0,45255	0.089666484
4152	PA4150_at	PA4150 /DEF=probable dehydrogenase E1 compone	-3.413666629	-82.85166667	24.27057931	0,45310	0.089666484
195	PA0180_at	PA0180 /DEF=probable chemotaxis transducer /FUN	-4.452665099	-43.1425	9.689141006	0,45314	0.089666484
229	PA0214_at	PA0214 /DEF=probable acyl transferase /FUNCTION	-4.907283212	-27.10833333	5.524102066	0,45514	0.089666484
1147	PA1132_at	PA1132 /DEF=hypothetical protein /FUNCTION=Hyp	-6.934054702	-40.44666667	5.833046955	0,45654	0.089666484
250	PA0235_pcaK_at	PA0235 /GENE=pcaK /DEF=4-hydroxybenzoate tran	-4.030824174	-56.6425	14.05233708	0,45656	0.089666484
2294	PA2285_at	PA2285 /DEF=hypothetical protein /FUNCTION=Hyp	-3.939456582	-42.3075	10.73942538	0,45894	0.089666484
150	PA0135_at	PA0135 /DEF=hypothetical protein /FUNCTION=Hyp	-4.270541709	-20.14166667	4.716419611	0,46062	0.089666484
2295	PA2286_at	PA2286 /DEF=hypothetical protein /FUNCTION=Men	-4.565428383	-37.13666667	8.134322467	0,46154	0.089666484
4197	PA4195_at	PA4195 /DEF=probable binding protein component o	-4.060929246	-43.7725	10.77893688	0,46463	0.089666484
4043	PA4041_at	PA4041 /DEF=hypothetical protein /FUNCTION=Put	-3.730666386	-27.84666667	7.464260748	0,46526	0.089666484
4086	PA4084_at	PA4084 /DEF=probable fimbrial biogenesis usher prc	-3.54476775	-17.80083333	5.021720629	0,46618	0.089666484
4321	PA4325_at	PA4325 /DEF=hypothetical protein /FUNCTION=Hyp	-4.416450853	-142.3491667	32.23157495	0,46626	0.089666484
2334	PA2327_at	PA2327 /DEF=probable permease of ABC transporte	-4.049906713	-52.3225	12.91943339	0,46630	0.089666484
235	PA0220_at	PA0220 /DEF=probable amino acid permease /FUNC	-4.456373074	-31.29083333	7.021591956	0,46891	0.089666484
2289	PA2280_at	PA2280 /DEF=conserved hypothetical protein /FUNC	-3.715139063	-20.095	5.408949613	0,46928	0.089666484
2932	PA2927_at	PA2927 /DEF=hypothetical protein /FUNCTION=Hyp	-4.737180867	-27.39166667	5.782271658	0,46932	0.089666484
1917	PA1905_s_at	PA1905 /DEF=probable pyridoxamine 5'-phosphate c	-3.405089928	-39.00333333	11.45442093	0,46932	0.089666484
167	PA0152_pcaQ_at	PA0152 /GENE=pcaQ /DEF=transcriptional regulator	-4.617472829	-41.42333333	8.970996661	0,46996	0.089666484
4793	PA4798_at	PA4798 /DEF=hypothetical protein /FUNCTION=Hyp	-4.061617451	-25.7325	6.335530195	0,47085	0.089666484
4784	PA4788_at	PA4788 /DEF=hypothetical protein /FUNCTION=Hyp	-3.38532173	-72.00833333	21.27075034	0,47129	0.089666484
2332	PA2325_at	PA2325 /DEF=hypothetical protein /FUNCTION=Put	-3.725552893	-32.58333333	8.745905444	0,47278	0.089666484
5178	PA5183_at	PA5183 /DEF=hypothetical protein /FUNCTION=Hyp	-5.578399852	-110.9641667	19.89175563	0,47426	0.089666484
192	PA0177_at	PA0177 /DEF=probable purine-binding chemotaxis pi	-3.904042522	-17.6	4.508147619	0,47473	0.089666484
4114	PA4112_at	PA4112 /DEF=probable sensor/response regulator h	-4.566562506	-61.49916667	13.46727798	0,47499	0.089666484

254	PA0239_at	PA0239 /DEF=hypothetical protein /FUNCTION=Hyp	-5.15934248	-48.89083333	9.476175215	0,47614	0.089666484
2934	PA2929_at	PA2929 /DEF=hypothetical protein /FUNCTION=Hyp	-5.036741315	-30.56916667	6.069234998	0,47632	0.089666484
1622	PA1608_at	PA1608 /DEF=probable chemotaxis transducer /FUN	-4.112025745	-37.3675	9.087370147	0,47794	0.089666484
2883	PA2878_at	PA2878 /DEF=hypothetical protein /FUNCTION=Hyp	-4.696962231	-20.15416667	4.290893917	0,47810	0.089666484
169	PA0154_pcaG_at	PA0154 /GENE=pcaG /DEF=protocatechuate 3,4-dio	-4.012539165	-115.0466667	28.6717866	0,47849	0.089666484
380	PA0365_at	PA0365 /DEF=hypothetical protein /FUNCTION=Hyp	-4.663559958	-44.8575	9.618724838	0,48016	0.089666484
2886	PA2881_at	PA2881 /DEF=probable two-component response rec	-3.915233064	-27.1975	6.946585185	0,48024	0.089666484
3876	PA3872_narI_at	PA3872 /GENE=narI /DEF=respiratory nitrate reduct	-3.879930487	-51.63666667	13.30865768	0,48063	0.089666484
3467	PA3463_at	PA3463 /DEF=conserved hypothetical protein /FUNC	-3.662660778	-128.2875	35.02576618	0,48120	0.089666484
4041	PA4039_at	PA4039 /DEF=hypothetical protein /FUNCTION=Hyp	-3.317121611	-16.4175	4.949321105	0,48193	0.089666484
400	PA0385_at	PA0385 /DEF=hypothetical protein /FUNCTION=Hyp	-4.06954114	-23.35666667	5.739385808	0,48234	0.089666484
3889	PA3885_at	PA3885 /DEF=hypothetical protein /FUNCTION=Hyp	-5.84448636	-45.96666667	7.864962605	0,48312	0.089666484
4109	PA4107_at	PA4107 /DEF=hypothetical protein /FUNCTION=Hyp	-3.466398257	-40.46666667	11.67398079	0,48359	0.089666484
4831	PA4836_at	PA4836 /DEF=hypothetical protein /FUNCTION=Hyp	-3.967187244	-24.09083333	6.072522382	0,48419	0.089666484
2303	PA2295_at	PA2295 /DEF=probable permease of ABC transporte	-3.683800326	-16.19916667	4.397406274	0,48419	0.089666484
4813	PA4818_at	PA4818 /DEF=conserved hypothetical protein /FUNC	-4.011618021	-41.68166667	10.39023817	0,48420	0.089666484
189	PA0174_at	PA0174 /DEF=conserved hypothetical protein /FUNC	-4.31660619	-28.10166667	6.510129817	0,48501	0.089666484
2345	PA2338_at	PA2338 /DEF=probable binding protein component o	-3.728068665	-29.88333333	8.015767953	0,48502	0.089666484
4356	PA4360_at	PA4360 /DEF=hypothetical protein /FUNCTION=Hyp	-3.815198311	-257.39	67.46438298	0,48593	0.089666484
1868	PA1854_at	PA1854 /DEF=conserved hypothetical protein /FUNC	-3.56720052	-23.72416667	6.650640056	0,48613	0.089666484
393	PA0378_at	PA0378 /DEF=probable transglycosylase /FUNCTION=	-5.427928061	-31.79166667	5.857053798	0,48641	0.089666484
1693	PA1679_at	PA1679 /DEF=hypothetical protein /FUNCTION=Hyp	-5.586562372	-37.27083333	6.671514762	0,48766	0.089666484
2269	PA2260_at	PA2260 /DEF=hypothetical protein /FUNCTION=Hyp	-4.089756281	-30.485	7.453989408	0,48943	0.089666484
208	PA0193_at	PA0193 /DEF=hypothetical protein /FUNCTION=Hyp	-4.060622038	-18.24083333	4.492127847	0,48954	0.089666484
4581	PA4585_rtcA_at	PA4585 /GENE=rtcA /DEF=RNA 3'-terminal phospho	-7.23052753	-39.34916667	5.442087939	0,49004	0.089666484
364	PA0349_at	PA0349 /DEF=hypothetical protein /FUNCTION=Hyp	-3.742327999	-17.90083333	4.783341635	0,49036	0.089666484
4888	PA4893_ureG_at	PA4893 /GENE=ureG /DEF=urease accessory protei	-3.726012026	-40.47	10.86147863	0,49077	0.089666484
2075	PA2066_at	PA2066 /DEF=hypothetical protein /FUNCTION=Hyp	-3.390444972	-54.5325	16.08417197	0,49342	0.089666484
3913	PA3909_at	PA3909 /DEF=hypothetical protein /FUNCTION=Hyp	-4.578763612	-42.87666667	9.364245526	0,49402	0.089666484
4877	PA4882_at	PA4882 /DEF=hypothetical protein /FUNCTION=Hyp	-3.884150369	-34.15166667	8.792570685	0,49503	0.089666484
2095	PA2086_at	PA2086 /DEF=probable epoxide hydrolase /FUNCTIO	-3.897440233	-26.51916667	6.804252299	0,49777	0.089666484
4880	PA4885_irlR_at	PA4885 /GENE=irlR /DEF=two-component response	-3.711858407	-33.29666667	8.970349355	0,49807	0.089666484
2941	PA2936_at	PA2936 /DEF=hypothetical protein /FUNCTION=Hyp	-3.805498112	-18.09416667	4.754743304	0,49837	0.089666484
4042	PA4040_at	PA4040 /DEF=hypothetical protein /FUNCTION=Hyp	-3.924306022	-31.22916667	7.957882615	0,49943	0.089666484

Significant Genes List - Table A2

P. aeruginosa mutator M25/M26 versus non-mutator isolate M1 of patient M

Input Parameters

Imputation Engine	10-Nearest Neighbor Imputer
Data Type	Two Class, unpaired data
Data in log scale?	FALSCH
Number of Permutations	100
Blocked Permutation?	FALSCH
RNG Seed	1234567
(Delta, Fold Change)	(2,25930, 2,00000)
(Upper Cutoff, Lower Cutoff)	(3,59397, -3,07141)

Computed Quantities

Computed Exchangeability Factor S0	0.070719096
S0 percentile	0
False Significant Number (Median, 90 percentile)	(0,31017, 7,44407)
False Discovery Rate (Median, 90 percentile)	(0,03746, 0,89904)
Pi0Hat	0,31017

293 Positive Significant Genes

Row	Gene Name	Gene ID	Score(d)	Numerator(r)	denominator(s+s)	Fold Change	q-value (%)
609	PA0594_surA_at	PA0594 /GENE=surA /DEF=peptidyl-prolyl cis-trans is	20.32300454	163.8283333	8.061226038	4,31323	0.037460084
3816	PA3812_iscA_at	PA3812 /GENE=iscA /DEF=probable iron-binding prot	15.03173227	308.8183333	20.54442747	3,33035	0.037460084
4665	PA4669_ipk_at	PA4669 /GENE=ipk /DEF=isopentenyl monophosphat	14.83577297	82.49833333	5.560770813	2,97585	0.037460084
1023	PA1008_bcp_at	PA1008 /GENE=bcp /DEF=bacterioferritin comigratory	14.17716382	158.0666667	11.14938564	2,25929	0.037460084
5547	PA5553_atpC_at	PA5553 /GENE=atpC /DEF=ATP synthase epsilon ch	14.14999829	168.745	11.92544314	3,09162	0.037460084
2563	PA2557_at	PA2557 /DEF=probable AMP-binding enzyme /FUNCT	13.90250695	52.135	3.750043082	2,13386	0.037460084
567	PA0552_pgk_at	PA0552 /GENE=pgk /DEF=phosphoglycerate kinase /I	12.9024466	201.3666667	15.60685914	2,70659	0.037460084
1807	PA1793_ppiB_at	PA1793 /GENE=ppiB /DEF=peptidyl-prolyl cis-trans is	12.30596374	477.3633333	38.7912189	3,19400	0.037460084
2618	PA2612_serS_at	PA2612 /GENE=serS /DEF=seryl-tRNA synthetase /FI	12.1747264	120.74	9.917265988	2,04764	0.037460084
2186	PA2177_at	PA2177 /DEF=probable sensor/response regulator hy	12.08477179	23.17166667	1.917426913	2,26806	0.037460084
2120	PA2111_at	PA2111 /DEF=hypothetical protein /FUNCTION=Hypo	11.47118728	1408.445	122.7811007	10,27056	0.037460084

977 PA0962_at	PA0962 /DEF=probable dna-binding stress protein /FL	11.44974994	840.495	73.40728002	4,32795	0.037460084
989 PA0974_at	PA0974 /DEF=conserved hypothetical protein /FUNCT	10.48610688	152.8483333	14.57627078	3,13993	0.037460084
985 PA0970_tolR_at	PA0970 /GENE=tolR /DEF=ToIR protein /FUNCTION=	10.16306878	273.6633333	26.92723422	3,52955	0.037460084
5004 PA5009_waaP_a	PA5009 /GENE=waaP /DEF=lipopolysaccharide core l	10.10807117	65.56166667	6.48607094	2,01321	0.037460084
986 PA0971_tolA_at	PA0971 /GENE=tolA /DEF=ToIA protein /FUNCTION=	10.04420817	234.9883333	23.39540653	4,27753	0.037460084
2121 PA2112_at	PA2112 /DEF=conserved hypothetical protein /FUNCT	9.977094381	1406.891667	141.0121638	9,53092	0.037460084
5429 PA5435_at	PA5435 /DEF=probable transcarboxylase subunit /FU	9.902418923	435.5333333	43.98251949	4,13913	0.037460084
83 PA0068_at	PA0068 /DEF=hypothetical protein /FUNCTION=Hypo	9.814257272	114.2583333	11.64207644	2,01995	0.037460084
5143 PA5148_at	PA5148 /DEF=conserved hypothetical protein /FUNCT	9.791308844	298.9816667	30.53541375	2,65129	0.037460084
4682 PA4686_at	PA4686 /DEF=hypothetical protein /FUNCTION=Hypo	9.779591227	113.5683333	11.6127894	3,32357	0.037460084
3807 PA3803_at	PA3803 /DEF=conserved hypothetical protein /FUNCT	9.690234315	186.2283333	19.21814554	2,79751	0.037460084
3168 PA3163_cmk_at	PA3163 /GENE=cmk /DEF=cytidylate kinase /FUNCTI	9.611813599	68.16166667	7.091446995	4,09123	0.037460084
2620 PA2614_lolA_at	PA2614 /GENE=lolA /DEF=periplasmic chaperone Lol	9.500040147	228.755	24.07937193	2,87085	0.037460084
3805 PA3801_at	PA3801 /DEF=conserved hypothetical protein /FUNCT	9.485726816	276.4666667	29.14554383	2,47880	0.037460084
4737 PA4741_rpsO_at	PA4741 /GENE=rpsO /DEF=30S ribosomal protein S1	9.438070638	486.275	51.5227125	2,26331	0.037460084
3073 PA3068_at	PA3068 /DEF=conserved hypothetical protein /FUNCT	9.421968323	634.4083333	67.33288752	4,27172	0.037460084
1601 PA1587_lpdG_at	PA1587 /GENE=lpdG /DEF=lipoamide dehydrogenase	9.403767369	174.8516667	18.59378904	3,11864	0.037460084
117 PA0102_at	PA0102 /DEF=probable carbonic anhydrase /FUNCTI	9.321921286	317.1666667	34.02374435	2,47705	0.037460084
5159 PA5164_rmlC_at	PA5164 /GENE=rmlC /DEF=dTDP-4-dehydrorhamnos	9.321865796	197.6766667	21.20569755	2,71629	0.037460084
2715 PA2710_at	PA2710 /DEF=hypothetical protein /FUNCTION=Hypo	9.318207318	73.17	7.852368755	2,55957	0.037460084
1576 PA1562_acnA_at	PA1562 /GENE=acnA /DEF=aconitate hydratase 1 /FL	9.281659977	70.82666667	7.630818931	2,98784	0.037460084
136 PA0121_at	PA0121 /DEF=hypothetical protein /FUNCTION=Hypo	9.270758517	1202.44	129.70244	15,29434	0.037460084
4555 PA4559_lspA_at	PA4559 /GENE=lspA /DEF=prolipoprotein signal pepti	9.216284518	85.60333333	9.288269385	3,02819	0.037460084
1019 PA1004_nadA_a	PA1004 /GENE=nadA /DEF=quinolinate synthetase A	9.130791631	119.6566667	13.10474179	2,43090	0.037460084
1354 PA1339_at	PA1339 /DEF=probable ATP-binding component of AE	9.089681933	231.3783333	25.45505278	3,42019	0.037460084
5165 PA5170_arcD_at	PA5170 /GENE=arcD /DEF=arginine/ornithine antiport	9.059982395	1752.403333	193.4223773	5,32692	0.037460084
2651 PA2645_nuoJ_at	PA2645 /GENE=nuoJ /DEF=NADH dehydrogenase I c	9.024124138	114.26	12.6616166	4,25465	0.037460084
1547 PA1533_at	PA1533 /DEF=conserved hypothetical protein /FUNCT	9.004340567	352.39	39.13556994	3,08137	0.037460084
5556 PA5562_spoOJ_	PA5562 /GENE=spoOJ /DEF=chromosome partitionin	8.932450212	158.3116667	17.72320729	2,63062	0.037460084
885 PA0870_phhC_a	PA0870 /GENE=phhC /DEF=aromatic amino acid ami	8.820120479	631.5233333	71.60030691	4,36998	0.037460084
497 PA0482_glcB_at	PA0482 /GENE=glcB /DEF=malate synthase G /FUNC	8.804871663	856.5816667	97.28496899	4,77088	0.037460084
3813 PA3809_fdx2_at	PA3809 /GENE=fdx2 /DEF=ferredoxin [2Fe-2S] /FUNC	8.701298147	200.53	23.04598654	2,52498	0.037460084
4534 PA4538_ndh_at	PA4538 /GENE=ndh /DEF=NADH dehydrogenase /FU	8.639635087	83.22666667	9.633122908	2,57865	0.037460084
2649 PA2643_nuoH_a	PA2643 /GENE=nuoH /DEF=NADH dehydrogenase I c	8.594055443	267.0733333	31.0765197	4,24341	0.037460084
5333 PA5339_at	PA5339 /DEF=conserved hypothetical protein /FUNCT	8.526415433	654.2416667	76.7311506	4,38576	0.037460084
3842 PA3838_at	PA3838 /DEF=probable ATP-binding component of AE	8.462554785	126.5133333	14.94978013	3,06440	0.037460084

4824	PA4829_lpd3_at	PA4829 /GENE=lpd3 /DEF=dihydrolipoamide dehydro	8.447335536	96.59166667	11.43457203	2,29589	0.037460084
2208	PA2199_at	PA2199 /DEF=probable dehydrogenase /FUNCTION=	8.428054572	108.5216667	12.87624157	5,91716	0.037460084
3172	PA3167_serC_at	PA3167 /GENE=serC /DEF=3-phosphoserine aminotr	8.373620136	103.595	12.37159058	2,97801	0.037460084
1979	PA1969_at	PA1969 /DEF=hypothetical protein /FUNCTION=Hypo	8.360115669	138.0383333	16.51153391	4,50707	0.037460084
678	PA0663_at	PA0663 /DEF=hypothetical protein /FUNCTION=Hypo	8.302156317	43.41833333	5.229765819	2,50288	0.037460084
1823	PA1809_at	PA1809 /DEF=probable permease of ABC transporter	8.274025669	38.17166667	4.613433435	2,32326	0.037460084
2647	PA2641_nuoF_at	PA2641 /GENE=nuoF /DEF=NADH dehydrogenase I c	8.21088019	158.4816667	19.30142238	3,76872	0.037460084
3051	PA3046_at	PA3046 /DEF=conserved hypothetical protein /FUNCT	8.20995923	152	18.51409925	2,65842	0.037460084
2206	PA2197_at	PA2197 /DEF=conserved hypothetical protein /FUNCT	8.208968578	140.2616667	17.08639342	10,30529	0.037460084
4556	PA4560_ileS_at	PA4560 /GENE=ileS /DEF=isoleucyl-tRNA synthetase	8.153860267	141.945	17.40831893	2,77817	0.037460084
915	PA0900_at	PA0900 /DEF=hypothetical protein /FUNCTION=Hypo	8.132743301	455.4933333	56.00734174	3,44206	0.037460084
3171	PA3166_pheA_a	PA3166 /GENE=pheA /DEF=chorismate mutase /FUN	8.104534885	94.74666667	11.69057423	2,51611	0.037460084
4691	PA4695_ilvH_at	PA4695 /GENE=ilvH /DEF=acetolactate synthase isoz	8.103884503	333.475	41.15001884	4,74131	0.037460084
3944	PA3940_at	PA3940 /DEF=probable DNA binding protein /FUNCTI	8.055629136	308.7233333	38.32392581	4,09870	0.037460084
3207	PA3202_at	PA3202 /DEF=conserved hypothetical protein /FUNCT	7.996988568	183.1616667	22.90383	2,59165	0.037460084
3974	PA3970_amn_at	PA3970 /GENE=amn /DEF=AMP nucleosidase /FUNC	7.90526728	73.40333333	9.285370214	2,52352	0.037460084
1822	PA1808_at	PA1808 /DEF=probable permease of ABC transporter	7.878363525	29.49833333	3.744220896	2,01976	0.037460084
319	PA0304_potI_at	PA0304 /GENE=potI /DEF=polyamine transport protei	7.850399024	33.72833333	4.296384583	2,07518	0.037460084
3806	PA3802_hisS_at	PA3802 /GENE=hisS /DEF=histidyl-tRNA synthetase /	7.770333673	124.53	16.0263388	3,16687	0.037460084
330	PA0315_at	PA0315 /DEF=hypothetical protein /FUNCTION=Hypo	7.727730208	309.465	40.0460409	2,77344	0.037460084
1832	PA1818_at	PA1818 /DEF=probable Orn/Arg/Lys decarboxylase /F	7.721788251	149.605	19.37439815	3,84258	0.037460084
2119	PA2110_at	PA2110 /DEF=hypothetical protein /FUNCTION=Hypo	7.655076104	491.9333333	64.26237005	6,12644	0.037460084
2581	PA2575_at	PA2575 /DEF=hypothetical protein /FUNCTION=Hypo	7.641423985	147.7683333	19.3378006	4,14222	0.037460084
5005	PA5010_waaG_ε	PA5010 /GENE=waaG /DEF=UDP-glucose:(heptosyl)	7.63084488	96.24833333	12.6130638	2,31355	0.037460084
3535	PA3531_bfrB_at	PA3531 /GENE=bfrB /DEF=bacterioferritin /FUNCTIONI	7.575246791	245.41	32.39630427	6,61536	0.037460084
1594	PA1580_gltA_at	PA1580 /GENE=gltA /DEF=citrate synthase /FUNCTIONI	7.563362235	1156.16	152.8632325	5,65424	0.037460084
4003	PA4000_at	PA4000 /DEF=hypothetical protein /FUNCTION=Hypo	7.546922727	114.6766667	15.1951558	2,08209	0.037460084
3625	PA3621_fdxA_at	PA3621 /GENE=fdxA /DEF=ferredoxin I /FUNCTION=	7.510015134	130.015	17.31221545	3,29101	0.037460084
886	PA0871_phhB_a	PA0871 /GENE=phhB /DEF=pterin-4-alpha-carbinolan	7.476260592	934.9583333	125.0569482	5,59718	0.037460084
1820	PA1806_fabI_at	PA1806 /GENE=fabI /DEF=NADH-dependent enoyl-A	7.461270608	90.91166667	12.1844752	3,08354	0.037460084
3210	PA3205_at	PA3205 /DEF=hypothetical protein /FUNCTION=Hypo	7.45053373	283.1733333	38.00712051	3,99369	0.037460084
987	PA0972_tolB_at	PA0972 /GENE=tolB /DEF=ToIB protein /FUNCTION=	7.393334806	445.2616667	60.22474003	3,82276	0.037460084
4460	PA4464_ptsN_at	PA4464 /GENE=ptsN /DEF=nitrogen regulatory IIA prc	7.345689526	285.57	38.87586032	2,06974	0.037460084
5423	PA5429_aspA_at	PA5429 /GENE=aspA /DEF=aspartate ammonia-lyase	7.342369482	267.2583333	36.39946668	3,10561	0.037460084
4660	PA4664_hemK_ε	PA4664 /GENE=hemK /DEF=probable methyl transfer	7.291019022	108.455	14.87514978	2,79939	0.037460084
2711	PA2706_at	PA2706 /DEF=hypothetical protein /FUNCTION=Hypo	7.277989768	116.9366667	16.06716558	2,06668	0.037460084

608	PA0593_pdxA_at	PA0593 /GENE=pdxA /DEF=pyridoxal phosphate bios	7.226604083	52.925	7.323633534	2,35612	0.037460084
2207	PA2198_at	PA2198 /DEF=hypothetical protein /FUNCTION=Hypo	7.206040144	116.5983333	16.18063888	7,66784	0.037460084
154	PA0139_ahpC_a	PA0139 /GENE=ahpC /DEF=alkyl hydroperoxide redu	7.182462288	990.9133333	137.962901	2,00924	0.037460084
1544	PA1530_at	PA1530 /DEF=hypothetical protein /FUNCTION=Hypo	7.124071131	62.235	8.735875718	2,48793	0.037460084
3985	PA3981_at	PA3981 /DEF=conserved hypothetical protein /FUNCT	7.072133583	88.86333333	12.56527925	2,10134	0.037460084
1809	PA1795_cysS_at	PA1795 /GENE=cysS /DEF=cysteinyl-tRNA synthetas	7.020237792	92.31666667	13.15007688	3,61767	0.037460084
2650	PA2644_nuol_at	PA2644 /GENE=nuol /DEF=NADH Dehydrogenase I c	7.017948015	167.3383333	23.84433925	3,54791	0.037460084
1789	PA1775_at	PA1775 /DEF=conserved hypothetical protein /FUNCT	7.014074088	93.62	13.34744955	2,68888	0.037460084
438	PA0423_at	PA0423 /DEF=conserved hypothetical protein /FUNCT	7.008140414	164.9016667	23.53001751	3,04373	0.037460084
2652	PA2646_nuoK_a	PA2646 /GENE=nuoK /DEF=NADH dehydrogenase I c	6.958667302	207.1433333	29.76767308	4,80522	0.037460084
1817	PA1803_lon_at	PA1803 /GENE=lon /DEF=Lon protease /FUNCTION=	6.88030496	351.725	51.12055382	3,59002	0.037460084
5013	PA5018_msrA_a	PA5018 /GENE=msrA /DEF=peptide methionine sulfo	6.864479432	149.2633333	21.74430484	2,38365	0.037460084
1372	PA1357_at	PA1357 /DEF=conserved hypothetical protein /FUNCT	6.819230336	37.885	5.55561231	2,25752	0.037460084
135	PA0120_at	PA0120 /DEF=probable transcriptional regulator /FUN	6.802143026	1351.7	198.716786	13,86721	0.037460084
4002	PA3999_dacC_a	PA3999 /GENE=dacC /DEF=D-ala-D-ala-carboxypepti	6.774106226	288.0583333	42.52344497	2,29715	0.037460084
4572	PA4576_at	PA4576 /DEF=probable ATP-dependent protease /FUL	6.743872786	65.39333333	9.696703275	2,28617	0.037460084
3836	PA3832_holC_at	PA3832 /GENE=holC /DEF=DNA polymerase III, chi s	6.742883205	33.20833333	4.924945654	2,72990	0.037460084
5003	PA5008_at	PA5008 /DEF=hypothetical protein /FUNCTION=Putat	6.738282069	83.81666667	12.43887771	2,24517	0.037460084
3820	PA3816_cysE_at	PA3816 /GENE=cysE /DEF=O-acetylserine synthase /	6.702548091	81.00166667	12.08520485	2,66888	0.037460084
3464	PA3460_at	PA3460 /DEF=probable acetyltransferase /FUNCTION	6.661004921	248.265	37.27140318	3,34759	0.037460084
2189	PA2180_at	PA2180 /DEF=hypothetical protein /FUNCTION=Hypo	6.65761947	15.97833333	2.400007	2,20926	0.037460084
1028	PA1013_purC_at	PA1013 /GENE=purC /DEF=phosphoribosylaminoimid	6.655258225	146.7816667	22.05499196	4,26859	0.037460084
5255	PA5260_hemC_ε	PA5260 /GENE=hemC /DEF=prophobilinogen deamin	6.610545673	86.55333333	13.09322068	2,26917	0.037460084
2646	PA2640_nuoE_a	PA2640 /GENE=nuoE /DEF=NADH dehydrogenase I c	6.586802762	285.0233333	43.27187919	2,65014	0.037460084
918	PA0903_alaS_at	PA0903 /GENE=alaS /DEF=alanyl-tRNA synthetase /F	6.519547596	65.23333333	10.00580675	2,19958	0.037460084
19	PA0004_gyrB_at	PA0004 /GENE=gyrB /DEF=DNA gyrase subunit B /FL	6.481862019	128.44	19.81529376	3,26326	0.037460084
913	PA0898_aruD_at	PA0898 /GENE=aruD /DEF=succinylglutamate 5-semi	6.40488123	89.48	13.97059474	2,31389	0.037460084
887	PA0872_phhA_a	PA0872 /GENE=phhA /DEF=phenylalanine-4-hydroxyl	6.356491168	1260.27	198.2650438	14,68322	0.037460084
2174	PA2165_at	PA2165 /DEF=probable glycogen synthase /FUNCTIO	6.342654161	29.38	4.632130218	2,54469	0.037460084
2118	PA2109_at	PA2109 /DEF=hypothetical protein /FUNCTION=Hypo	6.32502714	154.8883333	24.48816897	2,06506	0.037460084
2654	PA2648_nuoM_a	PA2648 /GENE=nuoM /DEF=NADH dehydrogenase I c	6.273226483	101.11	16.11770279	3,87817	0.037460084
1390	PA1375_pdxB_at	PA1375 /GENE=pdxB /DEF=erythronate-4-phosphate	6.173691288	45.385	7.351355596	2,11038	0.037460084
1357	PA1342_at	PA1342 /DEF=probable binding protein component of	6.126970152	479.575	78.27278216	2,16102	0.037460084
1603	PA1589_sucD_at	PA1589 /GENE=sucD /DEF=succinyl-CoA synthetase	6.112454904	1091.44	178.5600086	2,23698	0.037460084
517	PA0502_at	PA0502 /DEF=probable biotin biosynthesis protein bio	5.996021845	68.91166667	11.49289787	2,54418	0.037460084
4239	PA4242_rpmJ_at	PA4242 /GENE=rpmJ /DEF=50S ribosomal protein L3	5.908842918	1253.556667	212.1492624	2,10786	0.037460084

919	PA0904_lysC_at	PA0904 /GENE=lysC /DEF=aspartate kinase alpha an	5.891469927	126.73	21.51076074	3,16966	0.037460084
4001	PA3998_at	PA3998 /DEF=conserved hypothetical protein /FUNCT	5.86468149	139.02	23.70461213	2,46198	0.037460084
4999	PA5004_at	PA5004 /DEF=probable glycosyl transferase /FUNCTI	5.857159857	80.88333333	13.80930951	2,31732	0.037460084
902	PA0887_acsA_at	PA0887 /GENE=acsA /DEF=acetyl-coenzyme A synth	5.815398682	919.0066667	158.0298647	4,87756	0.037460084
2673	PA2667_at	PA2667 /DEF=conserved hypothetical protein /FUNCT	5.804661478	409.5433333	70.5542149	2,07449	0.037460084
1214	PA1199_at	PA1199 /DEF=probable lipoprotein /FUNCTION=Mem	5.769087464	166.2	28.8087156	2,04395	0.037460084
1352	PA1337_ansB_at	PA1337 /GENE=ansB /DEF=glutaminase-asparaginas	5.742385359	266.0316667	46.32772795	2,46908	0.037460084
1598	PA1584_sdhB_at	PA1584 /GENE=sdhB /DEF=succinate dehydrogenase	5.730960884	438.9933333	76.6003018	3,18444	0.037460084
1353	PA1338_ggt_at	PA1338 /GENE=ggt /DEF=gamma-glutamyltranspeptid	5.730940124	99.24	17.3165306	2,17918	0.037460084
2028	PA2018_at	PA2018 /DEF=RND multidrug efflux transporter /FUNC	5.714543409	92.39833333	16.16897917	3,59473	0.037460084
3000	PA2995_nqrE_at	PA2995 /GENE=nqrE /DEF=Na+-translocating NADH:	5.668558711	78.98166667	13.93328899	2,09737	0.037460084
1600	PA1586_sucB_at	PA1586 /GENE=sucB /DEF=dihydrolipoamide succiny	5.665628448	316.72	55.90200679	2,88147	0.037460084
63	PA0048_at	PA0048 /DEF=probable transcriptional regulator /FUN	5.657710704	88.48166667	15.63912885	2,99074	0.037460084
2622	PA2616_trxB1_a	PA2616 /GENE=trxB1 /DEF=thioredoxin reductase 1 /	5.652407837	215.4066667	38.10883306	2,17614	0.037460084
306	PA0291_oprE_at	PA0291 /GENE=oprE /DEF=outer membrane porin Op	5.649353078	92.31	16.33992401	2,15769	0.037460084
4739	PA4743_rbfA_at	PA4743 /GENE=rbfA /DEF=ribosome-binding factor A	5.641660838	161.7516667	28.67093065	2,79957	0.037460084
3804	PA3800_at	PA3800 /DEF=conserved hypothetical protein /FUNCT	5.64093727	57.28	10.15434089	2,26679	0.037460084
17	PA0002_dnaN_a	PA0002 /GENE=dnaN /DEF=DNA polymerase III, beta	5.623551026	180.69	32.13094345	2,16522	0.037460084
5158	PA5163_rmlA_at	PA5163 /GENE=rmlA /DEF=glucose-1-phosphate thyn	5.621762434	131.5733333	23.40428556	2,02961	0.037460084
880	PA0865_hpd_at	PA0865 /GENE=hpD /DEF=4-hydroxyphenylpyruvate c	5.591376773	920.52	164.6320821	7,17965	0.037460084
2648	PA2642_nuoG_a	PA2642 /GENE=nuoG /DEF=NADH dehydrogenase I c	5.562031197	245.3966667	44.11997308	3,75592	0.037460084
1588	PA1574_at	PA1574 /DEF=conserved hypothetical protein /FUNCT	5.549085713	187.465	33.78304277	6,18432	0.037460084
3475	PA3471_at	PA3471 /DEF=probable malic enzyme /FUNCTION=C	5.473389881	306.4016667	55.98023772	3,29646	0.037460084
4461	PA4465_at	PA4465 /DEF=conserved hypothetical protein /FUNCT	5.46123911	140.3933333	25.70723063	2,26858	0.037460084
2770	PA2765_at	PA2765 /DEF=hypothetical protein /FUNCTION=Hypo	5.454969219	52.88	9.693913546	2,13024	0.037460084
5064	PA5069_tatB_at	PA5069 /GENE=tatB /DEF=translocation protein TatB	5.450649637	71.25833333	13.07336521	2,42232	0.037460084
4247	PA4250_rpsN_at	PA4250 /GENE=rpsN /DEF=30S ribosomal protein S1	5.394493316	1453.285	269.4015758	3,85922	0.037460084
2122	PA2113_at	PA2113 /DEF=probable porin /FUNCTION=Transport	5.393442492	834.9566667	154.8095985	6,01717	0.037460084
2655	PA2649_nuoN_a	PA2649 /GENE=nuoN /DEF=NADH dehydrogenase I c	5.374832629	74.50833333	13.86244716	3,65532	0.037460084
5522	PA5528_at	PA5528 /DEF=hypothetical protein /FUNCTION=Hypo	5.359517368	307.6566667	57.40380067	3,11788	0.037460084
1026	PA1011_at	PA1011 /DEF=hypothetical protein /FUNCTION=Hypo	5.329679605	161.315	30.26729784	2,47427	0.037460084
1355	PA1340_at	PA1340 /DEF=probable permease of ABC transporter	5.312316789	83.28333333	15.67740341	3,62475	0.037460084
2019	PA2009_hmgA_ε	PA2009 /GENE=hmgA /DEF=homogentisate 1,2-dioxy	5.275406044	459.0833333	87.02331716	4,94978	0.037460084
1780	PA1766_at	PA1766 /DEF=hypothetical protein /FUNCTION=Hypo	5.249599715	48.545	9.24737173	2,14619	0.037460084
5044	PA5049_rpmE_a	PA5049 /GENE=rpmE /DEF=50S ribosomal protein L3	5.235683081	383.535	73.25405187	8,92755	0.037460084
2746	PA2741_rplT_at	PA2741 /GENE=rplT /DEF=50S ribosomal protein L20	5.234629126	553.98	105.8298471	3,42025	0.037460084

3815	PA3811_hscB_at	PA3811 /GENE=hscB /DEF=heat shock protein HscB	5.220380478	45.86833333	8.786396609	2,74007	0.037460084
4690	PA4694_ilvC_at	PA4694 /GENE=ilvC /DEF=keto-acid reductoisomerase	5.220177098	406.17	77.80770505	4,56592	0.037460084
3817	PA3813_iscU_at	PA3813 /GENE=iscU /DEF=probable iron-binding protein	5.204617958	208.415	40.04424565	6,05004	0.037460084
980	PA0965_ruvC_at	PA0965 /GENE=ruvC /DEF=Holliday junction resolvase	5.159147486	45.69666667	8.857406537	2,30215	0.037460084
134	PA0119_at	PA0119 /DEF=probable dicarboxylate transporter /FUNCTION=Transporter	5.151218569	572.7566667	111.1885778	14,05577	0.037460084
910	PA0895_aruC_at	PA0895 /GENE=aruC /DEF=N-succinylglutamate 5-semialdehyde lyase	5.132921794	165.8883333	32.31850006	4,51309	0.037460084
1546	PA1532_dnaX_a	PA1532 /GENE=dnaX /DEF=DNA polymerase subunit	5.127822899	45.65166667	8.902738562	2,84850	0.037460084
5114	PA5119_glnA_at	PA5119 /GENE=glnA /DEF=glutamine synthetase /FUNCTION=Glutamine synthetase	5.114860391	252.9566667	49.45524361	2,41773	0.037460084
2972	PA2967_fabG_at	PA2967 /GENE=fabG /DEF=3-oxoacyl-[acyl-carrier-protein] synthase 3	5.109518804	296.5583333	58.04036441	5,56314	0.037460084
591	PA0576_rpoD_at	PA0576 /GENE=rpoD /DEF=sigma factor RpoD /FUNCTION=Sigma factor	5.109462838	407.495	79.75300201	3,84411	0.037460084
516	PA0501_bioF_at	PA0501 /GENE=bioF /DEF=8-amino-7-oxononanoate synthase	5.106501235	70.175	13.74228591	2,51982	0.037460084
5315	PA5321_dut_at	PA5321 /GENE=dut /DEF=deoxyuridine 5'-triphosphatase	5.101873276	54.02	10.5882677	2,18352	0.037460084
2621	PA2615_ftsK_at	PA2615 /GENE=ftsK /DEF=cell division protein FtsK /FUNCTION=Cell division protein	5.097257843	129.575	25.4205308	2,34647	0.037460084
2636	PA2630_at	PA2630 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical protein	5.086643125	42.84666667	8.423367948	2,27381	0.037460084
2460	PA2453_at	PA2453 /DEF=hypothetical protein /FUNCTION=Hypothetical protein	5.048397105	30.96333333	6.133299876	2,26622	0.037460084
2018	PA2008_fahA_at	PA2008 /GENE=fahA /DEF=fumarylacetoacetase /FUNCTION=Fumarylacetoacetase	5.041022531	835.745	165.7887849	4,69303	0.037460084
4710	PA4714_at	PA4714 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical protein	5.030311985	111	22.06622578	2,79157	0.037460084
2653	PA2647_nuoL_at	PA2647 /GENE=nuoL /DEF=NADH dehydrogenase I core subunit	5.009290394	93.06666667	18.57881243	4,12269	0.037460084
5334	PA5340_at	PA5340 /DEF=hypothetical protein /FUNCTION=Hypothetical protein	4.934548782	143.2783333	29.03575173	2,16452	0.037460084
4069	PA4067_oprG_at	PA4067 /GENE=oprG /DEF=outer membrane protein G	4.915556747	596.94	121.4389398	2,90836	0.037460084
2179	PA2170_at	PA2170 /DEF=hypothetical protein /FUNCTION=Hypothetical protein	4.907807776	24.33666667	4.958765253	2,51442	0.037460084
912	PA0897_aruG_at	PA0897 /GENE=aruG /DEF=arginine/ornithine succinyl-CoA lyase	4.862541012	126.2966667	25.97338847	3,08755	0.037460084
4937	PA4942_hflK_at	PA4942 /GENE=hflK /DEF=protease subunit HflK /FUNCTION=Protease	4.858569066	185.2616667	38.13091141	2,51622	0.037460084
988	PA0973_oprL_at	PA0973 /GENE=oprL /DEF=outer membrane protein C	4.850999563	503.4016667	103.772771	2,38996	0.037460084
3283	PA3278_at	PA3278 /DEF=hypothetical protein /FUNCTION=Hypothetical protein	4.819890752	212.815	44.15349039	5,09365	0.037460084
3923	PA3919_at	PA3919 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical protein	4.787911464	191.335	39.96210068	3,04563	0.037460084
1815	PA1801_clpP_at	PA1801 /GENE=clpP /DEF=ATP-dependent Clp protease	4.786653019	445.5283333	93.07721524	2,93950	0.037460084
979	PA0964_at	PA0964 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical protein	4.761651629	338.1966667	71.02507555	2,92961	0.037460084
3767	PA3763_purL_at	PA3763 /GENE=purL /DEF=phosphoribosylformylglycinamido transferase	4.755926025	60.77333333	12.77844378	2,01340	0.037460084
2971	PA2966_acpP_at	PA2966 /GENE=acpP /DEF=acyl carrier protein /FUNCTION=Acyl carrier protein	4.723967557	1178.35	249.4407478	3,63839	0.037460084
3824	PA3820_secF_at	PA3820 /GENE=secF /DEF=secretion protein SecF /FUNCTION=Secretion protein	4.668886281	231.7566667	49.6385332	6,58450	0.037460084
2185	PA2176_at	PA2176 /DEF=hypothetical protein /FUNCTION=Hypothetical protein	4.66229129	23.79666667	5.104071193	2,45427	0.037460084
1208	PA1193_at	PA1193 /DEF=hypothetical protein /FUNCTION=Hypothetical protein	4.642464167	31.71	6.830424288	2,02921	0.037460084
3239	PA3234_at	PA3234 /DEF=probable sodium:solute symporter /FUNCTION=Transporter	4.636021819	246.2816667	53.12349171	2,73320	0.037460084
1243	PA1228_at	PA1228 /DEF=hypothetical protein /FUNCTION=Hypothetical protein	4.622041924	86.105	18.62921224	2,48133	0.037460084
914	PA0899_aruB_at	PA0899 /GENE=aruB /DEF=succinylarginine dihydrolase	4.600185041	133.3366667	28.98506592	4,26326	0.037460084

2173	PA2164_at	PA2164 /DEF=probable glycosyl hydrolase /FUNCTION=	4.593828696	27.80666667	6.053048233	2,44952	0.037460084
3691	PA3687_ppc_at	PA3687 /GENE=ppc /DEF=phosphoenolpyruvate carb	4.589206863	162.4216667	35.39209966	2,18593	0.037460084
4234	PA4237_rplQ_at	PA4237 /GENE=rplQ /DEF=50S ribosomal protein L17	4.580658916	638.1683333	139.3180206	6,39966	0.037460084
2169	PA2160_at	PA2160 /DEF=probable glycosyl hydrolase /FUNCTION=	4.562474055	34.10833333	7.475841599	2,98497	0.037460084
1585	PA1571_at	PA1571 /DEF=hypothetical protein /FUNCTION=Hypo	4.538862527	290.6666667	64.03953963	2,43698	0.037460084
4930	PA4935_rpsF_at	PA4935 /GENE=rpsF /DEF=30S ribosomal protein S6	4.527091791	1083.903333	239.4259678	6,56295	0.037460084
2801	PA2796_tal_at	PA2796 /GENE=tal /DEF=transaldolase /FUNCTION=	4.523934757	126.5166667	27.96606791	2,83926	0.037460084
3837	PA3833_at	PA3833 /DEF=hypothetical protein /FUNCTION=Hypo	4.508685667	47.61666667	10.561097	2,23690	0.037460084
515	PA0500_bioB_at	PA0500 /GENE=bioB /DEF=biotin synthase /FUNCTION=	4.50327129	183.3833333	40.72224867	3,10222	0.037460084
2029	PA2019_at	PA2019 /DEF=RND multidrug efflux membrane fusion	4.501579377	183.9033333	40.85306909	5,20607	0.037460084
317	PA0302_potG_at	PA0302 /GENE=potG /DEF=polyamine transport prote	4.444528516	70.66	15.89819927	2,14435	0.037460084
4229	PA4232_ssb_at	PA4232 /GENE=ssb /DEF=single-stranded DNA-bindin	4.444144175	190.14	42.78439054	3,31624	0.037460084
5613	Pae_AF241171α	AF241171 /GENE= /PROD= /FEATURE=cds21 /DEF=	4.437749894	31.77166667	7.159409031	3,59008	0.037460084
1529	PA1515_alc_at	PA1515 /GENE=alc /DEF=allantoicase /FUNCTION=C	4.419969794	63.61166667	14.39187814	2,13376	0.037460084
5218	PA5223_ubiH_at	PA5223 /GENE=ubiH /DEF=ubiH protein /FUNCTION=	4.376972891	88.63833333	20.25105833	2,00748	0.037460084
1599	PA1585_sucA_at	PA1585 /GENE=sucA /DEF=2-oxoglutarate dehydroge	4.360848804	131.4683333	30.14741837	3,43130	0.037460084
4262	PA4265_tufA_s_	PA4265 /GENE=tufA /DEF=elongation factor Tu /FUN	4.339055113	642.0183333	147.9627054	3,46456	0.037460084
2714	PA2709_cysK_at	PA2709 /GENE=cysK /DEF=cysteine synthase A /FUN	4.262687798	289.0566667	67.81089312	2,70713	0.037460084
5455	PA5461_at	PA5461 /DEF=hypothetical protein /FUNCTION=Hypo	4.243218857	321.5516667	75.78012765	5,00222	0.037460084
1784	PA1770_ppsA_at	PA1770 /GENE=ppsA /DEF=phosphoenolpyruvate syr	4.2289769	82.495	19.5070822	2,36808	0.037460084
137	PA0122_at	PA0122 /DEF=conserved hypothetical protein /FUNCT	4.227343861	350.33	82.87236892	3,98035	0.037460084
3835	PA3831_pepA_a	PA3831 /GENE=pepA /DEF=leucine aminopeptidase /	4.213350206	108.125	25.66247635	3,75735	0.037460084
4249	PA4252_rplX_at	PA4252 /GENE=rplX /DEF=50S ribosomal protein L24	4.203666793	2043.026667	486.010611	7,83843	0.037460084
2644	PA2638_nuoB_a	PA2638 /GENE=nuoB /DEF=NADH dehydrogenase I c	4.198351548	101.5933333	24.19838648	2,94412	0.037460084
1522	PA1507_at	PA1507 /DEF=probable transporter /FUNCTION=Merr	4.197175502	54.54666667	12.99604142	2,40996	0.037460084
1303	PA1288_at	PA1288 /DEF=probable outer membrane protein /FUN	4.192874153	629.95	150.2430021	2,03104	0.037460084
4693	PA4697_at	PA4697 /DEF=hypothetical protein /FUNCTION=Hypo	4.192781663	70.28	16.76214161	2,16306	0.037460084
4667	PA4671_at	PA4671 /DEF=probable ribosomal protein L25 /FUNC	4.190055754	1843.223333	439.9042498	4,13026	0.037460084
3774	PA3770_guaB_a	PA3770 /GENE=guaB /DEF=inosine-5'-monophosphat	4.182012841	176.2783333	42.15155238	3,99555	0.037460084
4268	PA4271_rplL_at	PA4271 /GENE=rplL /DEF=50S ribosomal protein L7 /	4.172811547	1588.078333	380.5775351	10,66376	0.037460084
3783	PA3779_at	PA3779 /DEF=hypothetical protein /FUNCTION=Hypo	4.165862715	50.91833333	12.22275836	2,23120	0.037460084
970	PA0955_at	PA0955 /DEF=hypothetical protein /FUNCTION=Hypo	4.156434124	83.65666667	20.12702816	2,06172	0.037460084
3773	PA3769_guaA_a	PA3769 /GENE=guaA /DEF=GMP synthase /FUNCTION=	4.153673582	331.9416667	79.9152028	4,41469	0.037460084
1610	PA1596_htpG_at	PA1596 /GENE=htpG /DEF=heat shock protein HtpG /	4.148936933	598.8933333	144.348623	2,91636	0.037460084
3579	PA3575_at	PA3575 /DEF=hypothetical protein /FUNCTION=Hypo	4.146947307	171.305	41.30869947	2,85368	0.037460084
4929	PA4934_rpsR_at	PA4934 /GENE=rpsR /DEF=30S ribosomal protein S1	4.127530365	1169.068333	283.2367614	5,26974	0.037460084

2125	PA2116_at	PA2116 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical protein	4.121101938	355.8633333	86.35149983	6,86556	0.037460084
3463	PA3459_at	PA3459 /DEF=probable glutamine amidotransferase /FUNCTION=Hypothetical protein	4.114609973	149.9083333	36.43318183	2,14065	0.037460084
2181	PA2172_at	PA2172 /DEF=hypothetical protein /FUNCTION=Hypothetical protein	4.099241817	17.65333333	4.306487424	2,40926	0.037460084
1566	PA1552_at	PA1552 /DEF=probable cytochrome c /FUNCTION=Electron transfer flavoprotein	4.09016721	447.0083333	109.288523	6,90864	0.037460084
2956	PA2951_etfA_at	PA2951 /GENE=etfA /DEF=electron transfer flavoprotein	4.068575947	660.6	162.3663927	2,43426	0.037460084
5046	PA5051_argS_at	PA5051 /GENE=argS /DEF=arginyl-tRNA synthetase	4.049227828	116.3433333	28.73222705	2,38487	0.037460084
2488	PA2482_at	PA2482 /DEF=probable cytochrome c /FUNCTION=Electron transfer flavoprotein	4.047344056	52.58333333	12.99205914	2,73925	0.037460084
1819	PA1805_ppiD_at	PA1805 /GENE=ppiD /DEF=peptidyl-prolyl cis-trans isomerase	4.046190732	127.8783333	31.60462317	2,10919	0.037460084
4697	PA4701_at	PA4701 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical protein	4.034219305	86.15833333	21.35687895	2,21321	0.037460084
2999	PA2994_nqrF_at	PA2994 /GENE=nqrF /DEF=Na+-translocating NADH dehydrogenase	4.022877352	47.76666667	11.87375664	2,52560	0.037460084
2172	PA2163_at	PA2163 /DEF=hypothetical protein /FUNCTION=Hypothetical protein	4.014426301	31.025	7.728377027	2,39188	0.037460084
4740	PA4744_infB_at	PA4744 /GENE=infB /DEF=translation initiation factor	4.009525334	228.5083333	56.99136788	2,99664	0.037460084
1527	PA1513_at	PA1513 /DEF=hypothetical protein /FUNCTION=Hypothetical protein	4.00184028	99.46166667	24.8539821	3,96223	0.037460084
4933	PA4938_purA_at	PA4938 /GENE=purA /DEF=adenylosuccinate synthetase	4.001798556	171.9283333	42.9627656	2,03116	0.037460084
4568	PA4572_fklB_at	PA4572 /GENE=fklB /DEF=peptidyl-prolyl cis-trans isomerase	3.995322997	81.42	20.37882796	2,16021	0.037460084
2629	PA2623_icd_at	PA2623 /GENE=icd /DEF=isocitrate dehydrogenase /FUNCTION=Hypothetical protein	3.977879935	831.5233333	209.0368103	2,33201	0.037460084
3746	PA3742_rplS_at	PA3742 /GENE=rplS /DEF=50S ribosomal protein L19	3.958886556	747.7083333	188.8683403	6,46105	0.037460084
2955	PA2950_at	PA2950 /DEF=hypothetical protein /FUNCTION=Hypothetical protein	3.949236936	258.3983333	65.42993939	3,64725	0.037460084
3018	PA3013_foaB_at	PA3013 /GENE=foaB /DEF=fatty-acid oxidation complex	3.928108176	117.9816667	30.03523869	2,14958	0.037460084
958	PA0943_at	PA0943 /DEF=hypothetical protein /FUNCTION=Hypothetical protein	3.922516103	229.0316667	58.38896786	3,88865	0.037460084
2835	PA2830_htpX_at	PA2830 /GENE=htpX /DEF=heat shock protein HtpX	3.920254876	137.14	34.98241934	3,18341	0.037460084
4526	PA4530_at	PA4530 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical protein	3.920059085	43.22833333	11.02746984	2,18575	0.037460084
1044	PA1029_at	PA1029 /DEF=hypothetical protein /FUNCTION=Hypothetical protein	3.90819399	97.59166667	24.97103954	2,20941	0.037460084
2030	PA2020_at	PA2020 /DEF=probable transcriptional regulator /FUNCTION=Hypothetical protein	3.891615622	367.425	94.41451462	5,74750	0.037460084
581	PA0566_at	PA0566 /DEF=hypothetical protein /FUNCTION=Hypothetical protein	3.888868341	49.35	12.69006705	2,08358	0.037460084
978	PA0963_aspS_at	PA0963 /GENE=aspS /DEF=aspartyl-tRNA synthetase	3.886512293	153.4466667	39.48184262	3,45057	0.037460084
4696	PA4700_mrcB_a	PA4700 /GENE=mrcB /DEF=penicillin-binding protein	3.879894179	55.39333333	14.27702169	2,05921	0.037460084
4235	PA4238_rpoA_at	PA4238 /GENE=rpoA /DEF=DNA-directed RNA polymerase	3.874247049	1570.355	405.3316632	4,37861	0.037460084
984	PA0969_tolQ_at	PA0969 /GENE=tolQ /DEF=TolQ protein /FUNCTION=Hypothetical protein	3.855863282	147.555	38.26769499	4,94638	0.037460084
3173	PA3168_gyrA_at	PA3168 /GENE=gyrA /DEF=DNA gyrase subunit A	3.853078613	76.68333333	19.90183462	2,42844	0.037460084
23	PA0008_glyS_at	PA0008 /GENE=glyS /DEF=glycyl-tRNA synthetase	3.835777479	80.82833333	21.07221646	2,13539	0.037460084
64	PA0049_at	PA0049 /DEF=hypothetical protein /FUNCTION=Hypothetical protein	3.827170687	302.01	78.91208016	10,31076	0.037460084
5489	PA5495_thrB_at	PA5495 /GENE=thrB /DEF=homoserine kinase	3.80529806	219.6633333	57.72565772	2,69080	0.037460084
3814	PA3810_hscA_at	PA3810 /GENE=hscA /DEF=heat shock protein HscA	3.782418558	38.755	10.24608975	2,37836	0.037460084
3113	PA3108_purF_at	PA3108 /GENE=purF /DEF=amidophosphoribosyltransferase	3.78159696	102.5983333	27.13095404	2,13737	0.037460084
4692	PA4696_ilvI_at	PA4696 /GENE=ilvI /DEF=acetolactate synthase large	3.779895335	150.7166667	39.8732381	3,31824	0.037460084

3690	PA3686_adk_at	PA3686 /GENE=adk /DEF=adenylate kinase /FUNCTION=Hypo	3.771886055	221.4266667	58.70449516	2,78412	0.037460084
5227	PA5232_at	PA5232 /DEF=conserved hypothetical protein /FUNCTION=Hypo	3.770341922	147.6933333	39.17239772	2,72653	0.037460084
2026	PA2016_at	PA2016 /DEF=probable transcriptional regulator /FUNCTION=Hypo	3.75987064	850.8283333	226.2919166	5,50094	0.037460084
4531	PA4535_at	PA4535 /DEF=hypothetical protein /FUNCTION=Hypo	3.759468108	83.97166667	22.33604974	2,70501	0.037460084
3537	PA3533_at	PA3533 /DEF=conserved hypothetical protein /FUNCTION=Hypo	3.735929123	199.8083333	53.48290258	2,41281	0.037460084
4266	PA4269_rpoC_at	PA4269 /GENE=rpoC /DEF=DNA-directed RNA polymerase /FUNCTION=Hypo	3.735142406	680.9583333	182.3112105	4,20074	0.037460084
4928	PA4933_at	PA4933 /DEF=hypothetical protein /FUNCTION=Hypo	3.735067164	542.9733333	145.3717723	9,00491	0.037460084
4381	PA4385_groEL_at	PA4385 /GENE=groEL /DEF=GroEL protein /FUNCTION=Hypo	3.72860952	1105.773333	296.5645309	2,37421	0.037460084
2744	PA2739_pheT_at	PA2739 /GENE=pheT /DEF=phenylalanyl-tRNA synthetase /FUNCTION=Hypo	3.723407298	37.11166667	9.967125189	2,29414	0.037460084
922	PA0907_at	PA0907 /DEF=hypothetical protein /FUNCTION=Hypo	3.722434552	107.415	28.85611513	2,70979	0.037460084
4671	PA4675_at	PA4675 /DEF=probable TonB-dependent receptor /FUNCTION=Hypo	3.719428059	117.26	31.52635248	3,90319	0.037460084
4554	PA4558_at	PA4558 /DEF=probable peptidyl-prolyl cis-trans isomerase /FUNCTION=Hypo	3.710301686	384.6083333	103.6595851	2,50787	0.037460084
519	PA0504_bioD_at	PA0504 /GENE=bioD /DEF=dethiobiotin synthase /FUNCTION=Hypo	3.693552778	56.58333333	15.31948688	2,18731	0.037460084
3739	PA3735_thrC_at	PA3735 /GENE=thrC /DEF=threonine synthase /FUNCTION=Hypo	3.681418658	102.03	27.71485927	2,60458	0.037460084
1307	PA1292_at	PA1292 /DEF=probable 3-mercaptopyruvate sulfurtransferase /FUNCTION=Hypo	3.680144723	34.57833333	9.395916719	2,10674	0.037460084
2630	PA2624_idh_at	PA2624 /GENE=idh /DEF=isocitrate dehydrogenase /FUNCTION=Hypo	3.679820136	889.1483333	241.6282048	10,24719	0.037460084
2973	PA2968_fabD_at	PA2968 /GENE=fabD /DEF=malonyl-CoA-acyl-carrier protein /FUNCTION=Hypo	3.6779956	67.045	18.22867868	4,19871	0.037460084
1215	PA1200_at	PA1200 /DEF=conserved hypothetical protein /FUNCTION=Hypo	3.673148232	158.4766667	43.14464232	3,57379	0.037460084
5552	PA5558_atpF_at	PA5558 /GENE=atpF /DEF=ATP synthase B chain /FUNCTION=Hypo	3.66397385	849.22	231.7756716	2,98046	0.037460084
4270	PA4273_rplA_at	PA4273 /GENE=rplA /DEF=50S ribosomal protein L1 /FUNCTION=Hypo	3.662872523	1045.233333	285.3589162	6,56459	0.037460084
5553	PA5559_atpE_at	PA5559 /GENE=atpE /DEF=atp synthase C chain /FUNCTION=Hypo	3.660155762	687.445	187.8185096	2,57922	0.037460084
5268	PA5274_rnk_at	PA5274 /GENE=rnk /DEF=nucleoside diphosphate kinase /FUNCTION=Hypo	3.650831394	160.2066667	43.88224199	2,47520	0.037460084
4238	PA4241_rpsM_at	PA4241 /GENE=rpsM /DEF=30S ribosomal protein S1 /FUNCTION=Hypo	3.641433758	1023.766667	281.1438391	6,95467	0.037460084
4425	PA4429_at	PA4429 /DEF=probable cytochrome c1 precursor /FUNCTION=Hypo	3.624367439	245.6083333	67.76584811	2,71442	0.037460084
2645	PA2639_nuoD_at	PA2639 /GENE=nuoD /DEF=NADH dehydrogenase I /FUNCTION=Hypo	3.61888247	114.1733333	31.54933444	4,09665	0.037460084
2180	PA2171_at	PA2171 /DEF=hypothetical protein /FUNCTION=Hypo	3.615141722	40.005	11.06595621	3,71896	0.037460084
2749	PA2744_thrS_at	PA2744 /GENE=thrS /DEF=threonyl-tRNA synthetase /FUNCTION=Hypo	3.601138611	118.8316667	32.99835955	4,25923	0.037460084
4231	PA4234_uvrA_at	PA4234 /GENE=uvrA /DEF=excinuclease ABC subunit /FUNCTION=Hypo	3.598738391	68.87333333	19.1381884	2,74348	0.037460084
3291	PA3286_at	PA3286 /DEF=hypothetical protein /FUNCTION=Hypo	3.596487913	168.9983333	46.98982381	3,02936	0.037460084
5430	PA5436_at	PA5436 /DEF=probable biotin carboxylase subunit of acetyl-CoA carboxylase /FUNCTION=Hypo	3.593965913	458.5716667	127.5948848	3,24061	0.037460084

521 Negative Significant Genes

Row	Gene Name	Gene ID	Score(d)	Numerator(r)	denominator(s+s)	Fold Change	q-value (%)
1775	PA1761_at	PA1761 /DEF=hypothetical protein /FUNCTION=Hypo	-44.39295378	-879.9033333	19.82078817	0,11870	0.037460084
195	PA0180_at	PA0180 /DEF=probable chemotaxis transducer /FUNCTION=Hypo	-43.04272313	-94.095	2.186083806	0,23750	0.037460084
4322	PA4326_at	PA4326 /DEF=hypothetical protein /FUNCTION=Hypo	-40.29132525	-399.8683333	9.924427426	0,06408	0.037460084

4920	PA4925_at	PA4925 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical protein	-38.23096467	-100.6933333	2.63381618	0,18756	0.037460084
4856	PA4861_at	PA4861 /DEF=probable ATP-binding component of ABC transporter	-36.95499697	-123.6216667	3.345194881	0,17349	0.037460084
1773	PA1759_at	PA1759 /DEF=probable transcriptional regulator /FUNCTION=Transcriptional regulator	-35.66755604	-43.35666667	1.215577165	0,40966	0.037460084
3530	PA3526_at	PA3526 /DEF=probable outer membrane protein /FUNCTION=Outer membrane protein	-32.16894907	-357.16	11.10263189	0,07142	0.037460084
3728	PA3724_lasB_at	PA3724 /GENE=lasB /DEF=elastase LasB /FUNCTION=Elastase	-28.12483159	-144.875	5.151141955	0,16537	0.037460084
125	PA0110_at	PA0110 /DEF=hypothetical protein /FUNCTION=Hypothetical protein	-26.99032178	-220.4083333	8.166198801	0,15575	0.037460084
1622	PA1608_at	PA1608 /DEF=probable chemotaxis transducer /FUNCTION=Chemotaxis transducer	-25.88132236	-88.49833333	3.419389941	0,20520	0.037460084
2300	PA2292_at	PA2292 /DEF=hypothetical protein /FUNCTION=Hypothetical protein	-24.63753421	-129.815	5.268993191	0,14408	0.037460084
4838	PA4843_at	PA4843 /DEF=probable two-component response regulator	-23.81137967	-175.6266667	7.375745089	0,17792	0.037460084
2305	PA2297_at	PA2297 /DEF=probable ferredoxin /FUNCTION=Energy-coupled ferredoxin	-23.07591097	-132.6483333	5.748346555	0,25893	0.037460084
126	PA0111_at	PA0111 /DEF=hypothetical protein /FUNCTION=Hypothetical protein	-21.89956174	-338.06	15.4368386	0,12969	0.037460084
4907	PA4912_at	PA4912 /DEF=probable permease of ABC branched chain amino acid transporter	-21.78319627	-49.20666667	2.258927756	0,29049	0.037460084
4097	PA4095_at	PA4095 /DEF=hypothetical protein /FUNCTION=Hypothetical protein	-21.21034821	-28.94166667	1.364506908	0,43259	0.037460084
2304	PA2296_at	PA2296 /DEF=hypothetical protein /FUNCTION=Hypothetical protein	-20.54212103	-42.14666667	2.051719324	0,37129	0.037460084
538	PA0523_norC_at	PA0523 /GENE=norC /DEF=nitric-oxide reductase subunit gamma	-20.26792199	-38.54833333	1.901938114	0,31664	0.037460084
193	PA0178_at	PA0178 /DEF=probable two-component sensor /FUNCTION=Two-component sensor	-20.22246052	-202.6416667	10.02062368	0,15754	0.037460084
3312	PA3307_r_at	PA3307 /DEF=hypothetical protein /FUNCTION=Hypothetical protein	-19.74948548	-402.3666667	20.37352655	0,14844	0.037460084
3878	PA3874_narH_at	PA3874 /GENE=narH /DEF=respiratory nitrate reductase	-19.73970115	-54.66666667	2.76937661	0,30458	0.037460084
4976	PA4981_at	PA4981 /DEF=probable amino acid permease /FUNCTION=Amino acid permease	-19.51319706	-71.66333333	3.672557251	0,26227	0.037460084
1489	PA1474_at	PA1474 /DEF=hypothetical protein /FUNCTION=Hypothetical protein	-19.14778871	-49.84666667	2.603259698	0,29312	0.037460084
1484	PA1469_at	PA1469 /DEF=hypothetical protein /FUNCTION=Hypothetical protein	-19.04809742	-44.77666667	2.350715963	0,39173	0.037460084
4306	PA4310_pctB_at	PA4310 /GENE=pctB /DEF=chemotactic transducer PctB	-18.44660481	-123.025	6.669248964	0,14718	0.037460084
2883	PA2878_at	PA2878 /DEF=hypothetical protein /FUNCTION=Hypothetical protein	-18.33911442	-30.835	1.681378898	0,37699	0.037460084
1042	PA1027_at	PA1027 /DEF=probable aldehyde dehydrogenase /FUNCTION=Aldehyde dehydrogenase	-18.26308265	-115.5283333	6.325784947	0,25432	0.037460084
1056	PA1041_at	PA1041 /DEF=probable outer membrane protein /FUNCTION=Outer membrane protein	-18.13720466	-1001.933333	55.24188276	0,11537	0.037460084
2517	PA2511_at	PA2511 /DEF=probable transcriptional regulator /FUNCTION=Transcriptional regulator	-18.06293954	-63.87333333	3.536153858	0,40283	0.037460084
5096	PA5101_at	PA5101 /DEF=hypothetical protein /FUNCTION=Hypothetical protein	-18.01300389	-218.9433333	12.15473747	0,25974	0.037460084
194	PA0179_at	PA0179 /DEF=probable two-component response regulator	-16.76717214	-820.725	48.94832553	0,06935	0.037460084
2931	PA2926_hisP_at	PA2926 /GENE=hisP /DEF=histidine transport protein	-16.29549537	-71.675	4.398454812	0,21766	0.037460084
1231	PA1216_at	PA1216 /DEF=hypothetical protein /FUNCTION=Hypothetical protein	-16.14976564	-22.30833333	1.381340994	0,45193	0.037460084
191	PA0176_at	PA0176 /DEF=probable chemotaxis transducer /FUNCTION=Chemotaxis transducer	-15.72693765	-350.9716667	22.316593	0,17871	0.037460084
2303	PA2295_at	PA2295 /DEF=probable permease of ABC transporter	-15.65312664	-33.60333333	2.14674896	0,31793	0.037460084
1693	PA1679_at	PA1679 /DEF=hypothetical protein /FUNCTION=Hypothetical protein	-15.4851038	-74.02166667	4.780185373	0,27725	0.037460084
190	PA0175_at	PA0175 /DEF=probable chemotaxis protein methyltransferase	-15.46553516	-89.34333333	5.776931249	0,23367	0.037460084
2095	PA2086_at	PA2086 /DEF=probable epoxide hydrolase /FUNCTION=Epoxide hydrolase	-15.45268126	-56.22666667	3.638634987	0,32783	0.037460084
3889	PA3885_at	PA3885 /DEF=hypothetical protein /FUNCTION=Hypothetical protein	-15.38681484	-57.72166667	3.75137202	0,45111	0.037460084

399	PA0384_at	PA0384 /DEF=hypothetical protein /FUNCTION=Hypo	-15.26599197	-143.2416667	9.383056598	0,19747	0.037460084
4891	PA4896_at	PA4896 /DEF=probable sigma-70 factor, ECF subfam	-15.23374889	-80.83166667	5.306091575	0,35997	0.037460084
4794	PA4799_at	PA4799 /DEF=hypothetical protein /FUNCTION=Hypo	-15.15773055	-27.89166667	1.840095163	0,44472	0.037460084
2887	PA2882_at	PA2882 /DEF=probable two-component sensor /FUNC	-15.13411403	-85.18333333	5.628564259	0,24821	0.037460084
3908	PA3904_i_at	PA3904 /DEF=hypothetical protein /FUNCTION=Hypo	-15.05107883	-69.325	4.605982121	0,19271	0.037460084
2527	PA2521_czcB_at	PA2521 /GENE=czcB /DEF=RND divalent metal cation	-15.01025089	-22.03666667	1.468107817	0,46200	0.037460084
2378	PA2371_at	PA2371 /DEF=probable ClpA/B-type protease /FUNCT	-14.77206584	-38.035	2.574792206	0,46930	0.037460084
2130	PA2121_at	PA2121 /DEF=probable transcriptional regulator /FUN	-14.54770134	-20.085	1.380630488	0,49942	0.037460084
3876	PA3872_narI_at	PA3872 /GENE=narI /DEF=respiratory nitrate reductas	-14.20054189	-76.78833333	5.407422755	0,37043	0.037460084
4819	PA4824_at	PA4824 /DEF=hypothetical protein /FUNCTION=Hypo	-14.18439445	-51.89333333	3.6584807	0,43767	0.037460084
1473	PA1458_at	PA1458 /DEF=probable two-component sensor /FUNC	-14.17623331	-221.8483333	15.64931449	0,40776	0.037460084
2340	PA2333_at	PA2333 /DEF=probable sulfatase /FUNCTION=Putativ	-14.13488503	-68.74333333	4.863381145	0,29313	0.037460084
4629	PA4633_at	PA4633 /DEF=probable chemotaxis transducer /FUNC	-14.0839138	-356.64	25.32250659	0,14626	0.037460084
2013	PA2003_bdhA_a	PA2003 /GENE=bdhA /DEF=3-hydroxybutyrate dehyd	-14.07222113	-86.28	6.131228268	0,35630	0.037460084
4905	PA4910_at	PA4910 /DEF=probable ATP-binding component of AE	-13.99200533	-179.8366667	12.85281576	0,21739	0.037460084
3223	PA3218_at	PA3218 /DEF=hypothetical protein /FUNCTION=Hypo	-13.93294315	-65.57666667	4.70659113	0,26582	0.037460084
4195	PA4193_at	PA4193 /DEF=probable permease of ABC transporter	-13.83509007	-74.36	5.374739134	0,20032	0.037460084
4569	PA4573_at	PA4573 /DEF=hypothetical protein /FUNCTION=Hypo	-13.77689673	-327.6333333	23.78135946	0,22752	0.037460084
250	PA0235_pcaK_at	PA0235 /GENE=pcaK /DEF=4-hydroxybenzoate trans	-13.72332409	-61.90666667	4.511054776	0,38266	0.037460084
2334	PA2327_at	PA2327 /DEF=probable permease of ABC transporter	-13.59308128	-107.0766667	7.877291723	0,31338	0.037460084
4855	PA4860_at	PA4860 /DEF=probable permease of ABC transporter	-13.55927713	-25.215	1.859612409	0,46282	0.037460084
4851	PA4856_at	PA4856 /DEF=probable sensor/response regulator hyk	-13.55346552	-325.8633333	24.04280534	0,32505	0.037460084
4980	PA4985_at	PA4985 /DEF=hypothetical protein /FUNCTION=Hypo	-13.32749157	-53.91666667	4.045522475	0,31147	0.037460084
2289	PA2280_at	PA2280 /DEF=conserved hypothetical protein /FUNCT	-13.27859172	-44.64	3.361802287	0,29068	0.037460084
4899	PA4904_vanA_at	PA4904 /GENE=vanA /DEF=vanillate O-demethylase	-13.23393744	-46.30833333	3.499210538	0,35902	0.037460084
4888	PA4893_ureG_at	PA4893 /GENE=ureG /DEF=urease accessory protein	-13.21752654	-73.78833333	5.582612837	0,34336	0.037460084
4778	PA4782_at	PA4782 /DEF=hypothetical protein /FUNCTION=Hypo	-13.19014445	-201.9716667	15.31231651	0,38541	0.037460084
2096	PA2087_at	PA2087 /DEF=hypothetical protein /FUNCTION=Hypo	-13.11364496	-25.01666667	1.907682169	0,44465	0.037460084
2081	PA2072_at	PA2072 /DEF=conserved hypothetical protein /FUNCT	-13.05642393	-39.01666667	2.988311874	0,37530	0.037460084
258	PA0243_at	PA0243 /DEF=probable transcriptional regulator /FUN	-13.04760762	-72.02	5.519785857	0,40348	0.037460084
2868	PA2863_lipH_at	PA2863 /GENE=lipH /DEF=lipase modulator protein /F	-13.02471917	-53.265	4.089531553	0,28711	0.037460084
2292	PA2283_at	PA2283 /DEF=hypothetical protein /FUNCTION=Hypo	-13.0145603	-30.00166667	2.305238592	0,40930	0.037460084
2321	PA2313_at	PA2313 /DEF=hypothetical protein /FUNCTION=Hypo	-12.9277398	-61.26833333	4.739291963	0,21685	0.037460084
255	PA0240_at	PA0240 /DEF=probable porin /FUNCTION=Membrane	-12.86082303	-26.54	2.063631537	0,45774	0.037460084
4880	PA4885_irlR_at	PA4885 /GENE=irlR /DEF=two-component response r	-12.83551424	-67.90333333	5.290269797	0,31258	0.037460084
2066	PA2057_at	PA2057 /DEF=hypothetical protein /FUNCTION=Hypo	-12.8212443	-30.70166667	2.394593375	0,39742	0.037460084

2567	PA2561_at	PA2561 /DEF=probable chemotaxis transducer /FUNCTION=Hypo	-12.77056688	-59.65666667	4.671418835	0,31976	0.037460084
3626	PA3622_rpoS_at	PA3622 /GENE=rpoS /DEF=sigma factor RpoS /FUNCTION=Hypo	-12.75317166	-922.2666667	72.31665123	0,43079	0.037460084
3354	PA3349_at	PA3349 /DEF=probable chemotaxis protein /FUNCTION=Hypo	-12.70381297	-272.1416667	21.42204606	0,12716	0.037460084
364	PA0349_at	PA0349 /DEF=hypothetical protein /FUNCTION=Hypo	-12.59134271	-38.50333333	3.057921163	0,31517	0.037460084
2930	PA2925_hisM_at	PA2925 /GENE=hisM /DEF=histidine transport system /FUNCTION=Hypo	-12.54174327	-21.84666667	1.741916271	0,47438	0.037460084
3744	PA3740_at	PA3740 /DEF=hypothetical protein /FUNCTION=Hypo	-12.53828216	-76.425	6.095332598	0,21771	0.037460084
3927	PA3923_at	PA3923 /DEF=hypothetical protein /FUNCTION=Hypo	-12.51802503	-368.9083333	29.4701706	0,05437	0.037460084
412	PA0397_at	PA0397 /DEF=probable cation efflux system protein /FUNCTION=Hypo	-12.43256188	-21.88	1.759894719	0,46958	0.037460084
4772	PA4776_at	PA4776 /DEF=probable two-component response regulator /FUNCTION=Hypo	-12.42149749	-148.6266667	11.96527768	0,26335	0.037460084
5535	PA5541_at	PA5541 /DEF=probable dihydroorotase /FUNCTION=Hypo	-12.41058358	-29.895	2.408831124	0,41398	0.037460084
189	PA0174_at	PA0174 /DEF=conserved hypothetical protein /FUNCTION=Hypo	-12.39801268	-52.37833333	4.224736228	0,34456	0.037460084
2288	PA2279_arsC_at	PA2279 /GENE=arsC /DEF=ArsC protein /FUNCTION=Hypo	-12.3884169	-24.25	1.957473679	0,36623	0.037460084
791	PA0776_at	PA0776 /DEF=hypothetical protein /FUNCTION=Hypo	-12.3500384	-62.945	5.096745288	0,26409	0.037460084
4799	PA4804_at	PA4804 /DEF=probable amino acid permease /FUNCTION=Hypo	-12.23327401	-26.39166667	2.157367411	0,47403	0.037460084
168	PA0153_pcaH_a	PA0153 /GENE=pcaH /DEF=protocatechuate 3,4-dioxygenase /FUNCTION=Hypo	-12.20377946	-48.45833333	3.970764425	0,41232	0.037460084
2298	PA2289_at	PA2289 /DEF=conserved hypothetical protein /FUNCTION=Hypo	-12.11190037	-20.82666667	1.719520969	0,44576	0.037460084
4810	PA4815_at	PA4815 /DEF=hypothetical protein /FUNCTION=Hypo	-12.09837714	-43.74	3.615360927	0,47084	0.037460084
1872	PA1858_str_at	PA1858 /GENE=str /DEF=streptomycin 3"-phosphotransferase /FUNCTION=Hypo	-12.06561002	-29.16666667	2.417338751	0,46395	0.037460084
4859	PA4864_ureD_at	PA4864 /GENE=ureD /DEF=urease accessory protein /FUNCTION=Hypo	-12.05564566	-28.1	2.330858156	0,40696	0.037460084
1451	PA1436_at	PA1436 /DEF=probable RND efflux transporter /FUNCTION=Hypo	-11.97943677	-39.535	3.300238631	0,37809	0.037460084
4215	PA4218_at	PA4218 /DEF=probable transporter /FUNCTION=Membrane	-11.85030858	-356.4566667	30.07994807	0,25395	0.037460084
4221	PA4224_at	PA4224 /DEF=hypothetical protein /FUNCTION=Hypo	-11.73774173	-806.0566667	68.67221016	0,24820	0.037460084
401	PA0386_at	PA0386 /DEF=probable oxidase /FUNCTION=Putative	-11.70298571	-68.605	5.862179249	0,30423	0.037460084
3224	PA3219_at	PA3219 /DEF=hypothetical protein /FUNCTION=Hypo	-11.69806699	-93.945	8.030813989	0,30948	0.037460084
4793	PA4798_at	PA4798 /DEF=hypothetical protein /FUNCTION=Hypo	-11.69621936	-50.19166667	4.291272687	0,31607	0.037460084
230	PA0215_at	PA0215 /DEF=probable transporter /FUNCTION=Membrane	-11.6373838	-95.39833333	8.197575587	0,26046	0.037460084
393	PA0378_at	PA0378 /DEF=probable transglycosylase /FUNCTION=Hypo	-11.60337898	-43.25166667	3.727506164	0,41560	0.037460084
3881	PA3877_narK1_at	PA3877 /GENE=narK1 /DEF=nitrite extrusion protein /FUNCTION=Hypo	-11.57569491	-25.51833333	2.204475285	0,41382	0.037460084
4354	PA4358_at	PA4358 /DEF=probable ferrous iron transport protein /FUNCTION=Hypo	-11.55873447	-119.36	10.32639	0,30910	0.037460084
5321	PA5327_at	PA5327 /DEF=probable oxidoreductase /FUNCTION=Hypo	-11.49424678	-25.57333333	2.22488118	0,46540	0.037460084
4801	PA4806_at	PA4806 /DEF=probable transcriptional regulator /FUNCTION=Hypo	-11.46288897	-23.06	2.01170927	0,45885	0.037460084
2074	PA2065_pcoA_at	PA2065 /GENE=pcoA /DEF=copper resistance protein /FUNCTION=Hypo	-11.43075623	-26.965	2.358986531	0,43311	0.037460084
2076	PA2067_at	PA2067 /DEF=probable hydrolase /FUNCTION=Putative	-11.42382438	-49.43666667	4.327505834	0,37380	0.037460084
3995	PA3991_at	PA3991 /DEF=hypothetical protein /FUNCTION=Hypo	-11.38209544	-15.53	1.364423632	0,49752	0.037460084
813	PA0798_at	PA0798 /DEF=probable methyltransferase /FUNCTION=Hypo	-11.30257009	-32.41833333	2.868226702	0,44029	0.037460084
411	PA0396_pilU_at	PA0396 /GENE=pilU /DEF=twitching motility protein PilU /FUNCTION=Hypo	-11.28497076	-65.765	5.827662419	0,40568	0.037460084

3433	PA3428_at	PA3428 /DEF=hypothetical protein /FUNCTION=Hypo	-11.25670347	-56.735	5.040107891	0,32195	0.037460084
2347	PA2340_at	PA2340 /DEF=probable binding-protein-dependent ma	-11.25164834	-29.795	2.648056454	0,34252	0.037460084
1893	PA1879_at	PA1879 /DEF=hypothetical protein /FUNCTION=Hypo	-11.2410032	-39.67	3.529044454	0,40510	0.037460084
4773	PA4777_at	PA4777 /DEF=probable two-component sensor /FUNC	-11.19956036	-39.86666667	3.55966354	0,42228	0.037460084
398	PA0383_at	PA0383 /DEF=conserved hypothetical protein /FUNCT	-11.19913363	-26.675	2.381880677	0,42395	0.037460084
2037	PA2027_at	PA2027 /DEF=hypothetical protein /FUNCTION=Hypo	-11.17648642	-34.77833333	3.111741206	0,46390	0.037460084
2392	PA2385_at	PA2385 /DEF=probable acylase /FUNCTION=Putative	-11.14786467	-18.06666667	1.620639216	0,48863	0.037460084
3574	PA3570_mmsA_	PA3570 /GENE=mmsA /DEF=methylmalonate-semialc	-11.11223577	-1359.27	122.3219187	0,16668	0.037460084
1882	PA1868_xqhA_at	PA1868 /GENE=xqhA /DEF=secretion protein XqhA /F	-11.0528585	-49.20333333	4.451638764	0,45491	0.037460084
3255	PA3250_at	PA3250 /DEF=hypothetical protein /FUNCTION=Hypo	-10.98668644	-86.86833333	7.906690865	0,32058	0.037460084
2315	PA2307_at	PA2307 /DEF=probable permease of ABC transporter	-10.8967831	-19.32166667	1.773153277	0,49384	0.037460084
4854	PA4859_at	PA4859 /DEF=probable permease of ABC transporter	-10.71481864	-166.1216667	15.50391773	0,25977	0.037460084
4924	PA4929_at	PA4929 /DEF=hypothetical protein /FUNCTION=Hypo	-10.67213342	-104.6866667	9.809347629	0,18209	0.037460084
1652	PA1638_at	PA1638 /DEF=conserved hypothetical protein /FUNCT	-10.54912703	-32.89666667	3.118425493	0,49740	0.037460084
1894	PA1880_at	PA1880 /DEF=probable oxidoreductase /FUNCTION=	-10.43506492	-87.28666667	8.364745919	0,34812	0.037460084
2291	PA2282_at	PA2282 /DEF=hypothetical protein /FUNCTION=Hypo	-10.35040411	-83.025	8.021425937	0,26814	0.037460084
2084	PA2075_at	PA2075 /DEF=hypothetical protein /FUNCTION=Hypo	-10.3499435	-88.13	8.515022332	0,21259	0.037460084
5026	PA5031_at	PA5031 /DEF=probable short chain dehydrogenase /F	-10.34425516	-52.94833333	5.118622126	0,31000	0.037460084
2271	PA2262_at	PA2262 /DEF=probable 2-ketogluconate transporter /F	-10.33692582	-15.26166667	1.47642219	0,46891	0.037460084
234	PA0219_at	PA0219 /DEF=probable aldehyde dehydrogenase /FU	-10.31354317	-37.05166667	3.592525484	0,46527	0.037460084
5173	PA5178_at	PA5178 /DEF=conserved hypothetical protein /FUNCT	-10.29572801	-1749.951667	169.9687157	0,36805	0.037460084
2269	PA2260_at	PA2260 /DEF=hypothetical protein /FUNCTION=Hypo	-10.28801179	-63.77833333	6.19928657	0,31654	0.037460084
3390	PA3385_at	PA3385 /DEF=hypothetical protein /FUNCTION=Hypo	-10.28696053	-2765.513333	268.836779	0,27531	0.037460084
486	PA0471_at	PA0471 /DEF=probable transmembrane sensor /FUNC	-10.28314508	-50.58166667	4.918890695	0,49536	0.037460084
2068	PA2059_at	PA2059 /DEF=probable permease of ABC transporter	-10.26756251	-25.75333333	2.508222698	0,44545	0.037460084
4516	PA4520_at	PA4520 /DEF=probable chemotaxis transducer /FUNC	-10.24757159	-31.18333333	3.042997362	0,35089	0.037460084
254	PA0239_at	PA0239 /DEF=hypothetical protein /FUNCTION=Hypo	-10.24038901	-81.725	7.980653852	0,35741	0.037460084
1715	PA1701_at	PA1701 /DEF=conserved hypothetical protein in type I	-10.23607939	-94.88333333	9.269499553	0,21150	0.037460084
2658	PA2652_at	PA2652 /DEF=probable chemotaxis transducer /FUNC	-10.23173156	-69.165	6.759852875	0,27508	0.037460084
4227	PA4230_pchB_at	PA4230 /GENE=pchB /DEF=salicylate biosynthesis pr	-10.22855905	-601.7866667	58.8339632	0,16945	0.037460084
4820	PA4825_mgtA_at	PA4825 /GENE=mgtA /DEF=Mg(2+) transport ATPase	-10.19864667	-29.84166667	2.926041819	0,40853	0.037460084
3397	PA3392_nosZ_at	PA3392 /GENE=nosZ /DEF=nitrous-oxide reductase p	-10.13498316	-31.97833333	3.155242868	0,39826	0.037460084
4133	PA4131_at	PA4131 /DEF=probable iron-sulfur protein /FUNCTION	-10.07390497	-24.38	2.420114154	0,45966	0.037460084
4217	PA4220_i_at	PA4220 /DEF=hypothetical protein /FUNCTION=Hypo	-10.01148375	-419.98	41.94982589	0,20221	0.037460084
392	PA0377_at	PA0377 /DEF=hypothetical protein /FUNCTION=Hypo	-10.00940788	-175.35	17.51851879	0,32756	0.037460084
4893	PA4898_at	PA4898 /DEF=probable porin /FUNCTION=Membrane	-9.992008078	-115.925	11.60177205	0,21904	0.037460084

3926	PA3922_at	PA3922 /DEF=conserved hypothetical protein /FUNCTION=	-9.967532411	-819.425	82.20941415	0,08483	0.037460084
229	PA0214_at	PA0214 /DEF=probable acyl transferase /FUNCTION=	-9.951727054	-43.4	4.361052083	0,33653	0.037460084
1710	PA1696_pscO_a	PA1696 /GENE=pscO /DEF=translocation protein in ty	-9.948988924	-19.49666667	1.959663119	0,44690	0.037460084
1147	PA1132_at	PA1132 /DEF=hypothetical protein /FUNCTION=Hypo	-9.915867883	-44.17	4.454476453	0,42279	0.037460084
4305	PA4309_pctA_at	PA4309 /GENE=pctA /DEF=chemotactic transducer P	-9.885877083	-119.6933333	12.10750774	0,18570	0.037460084
4818	PA4823_at	PA4823 /DEF=hypothetical protein /FUNCTION=Hypo	-9.881581995	-82.66333333	8.365394668	0,20590	0.037460084
2920	PA2915_at	PA2915 /DEF=hypothetical protein /FUNCTION=Hypo	-9.849521767	-70.755	7.183597506	0,48368	0.037460084
4603	PA4607_at	PA4607 /DEF=hypothetical protein /FUNCTION=Hypo	-9.814907004	-2351.178333	239.5517688	0,30851	0.037460084
4586	PA4590_pra_at	PA4590 /GENE=pra /DEF=protein activator /FUNCTION	-9.732527264	-27.975	2.874381878	0,43534	0.037460084
4857	PA4862_at	PA4862 /DEF=probable ATP-binding component of AE	-9.72904404	-23.17666667	2.38221418	0,43167	0.037460084
4812	PA4817_at	PA4817 /DEF=hypothetical protein /FUNCTION=Hypo	-9.678436786	-155.8116667	16.09884634	0,29465	0.037460084
2268	PA2259_ptxS_at	PA2259 /GENE=ptxS /DEF=transcriptional regulator P	-9.672313652	-79.85833333	8.256383757	0,49258	0.037460084
1424	PA1409_aphA_a	PA1409 /GENE=aphA /DEF=acetylpolymine aminohy	-9.664118431	-25.07666667	2.594821954	0,46928	0.037460084
448	PA0433_at	PA0433 /DEF=hypothetical protein /FUNCTION=Hypo	-9.653601722	-49.31833333	5.108801332	0,32656	0.037460084
5411	PA5417_soxD_at	PA5417 /GENE=soxD /DEF=sarcosine oxidase delta s	-9.649253613	-25.225	2.614191834	0,46024	0.037460084
2884	PA2879_at	PA2879 /DEF=probable transcriptional regulator /FUN	-9.648842865	-57.89166667	5.999855887	0,48832	0.037460084
4833	PA4838_at	PA4838 /DEF=hypothetical protein /FUNCTION=Hypo	-9.58767764	-54.61	5.695852745	0,29179	0.037460084
1466	PA1451_at	PA1451 /DEF=conserved hypothetical protein /FUNCT	-9.480411456	-43.84	4.624271869	0,42202	0.037460084
208	PA0193_at	PA0193 /DEF=hypothetical protein /FUNCTION=Hypo	-9.474091663	-28.95666667	3.056405584	0,36845	0.037460084
2932	PA2927_at	PA2927 /DEF=hypothetical protein /FUNCTION=Hypo	-9.431681055	-44.145	4.680501783	0,35068	0.037460084
4197	PA4195_at	PA4195 /DEF=probable binding protein component of	-9.420316015	-52.83	5.608092119	0,41147	0.037460084
2085	PA2076_at	PA2076 /DEF=probable transcriptional regulator /FUN	-9.415970117	-108.3216667	11.50403679	0,23428	0.037460084
2285	PA2276_at	PA2276 /DEF=probable transcriptional regulator /FUN	-9.409291413	-63.785	6.778937669	0,31266	0.037460084
167	PA0152_pcaQ_a	PA0152 /GENE=pcaQ /DEF=transcriptional regulator f	-9.407201904	-68.43166667	7.274391192	0,36614	0.037460084
235	PA0220_at	PA0220 /DEF=probable amino acid permease /FUNC	-9.374798103	-50.805	5.419316709	0,34835	0.037460084
127	PA0112_at	PA0112 /DEF=hypothetical protein /FUNCTION=Hypo	-9.358214287	-128.5233333	13.7337455	0,26150	0.037460084
4114	PA4112_at	PA4112 /DEF=probable sensor/response regulator hy	-9.340219726	-111.6733333	11.9561784	0,33873	0.037460084
4883	PA4888_at	PA4888 /DEF=conserved hypothetical protein /FUNCT	-9.331757521	-35.24	3.776351874	0,46655	0.037460084
1189	PA1174_napA_a	PA1174 /GENE=napA /DEF=periplasmic nitrate reduct	-9.327937324	-46.80833333	5.018079744	0,49938	0.037460084
224	PA0209_at	PA0209 /DEF=conserved hypothetical protein /FUNCT	-9.270676386	-116.0183333	12.51454894	0,25281	0.037460084
2099	PA2090_at	PA2090 /DEF=hypothetical protein /FUNCTION=Hypo	-9.25176752	-32.17166667	3.477353554	0,39512	0.037460084
2872	PA2867_at	PA2867 /DEF=probable chemotaxis transducer /FUNC	-9.171181454	-380.0133333	41.43559205	0,13987	0.037460084
4086	PA4084_at	PA4084 /DEF=probable fimbrial biogenesis usher prot	-9.169075986	-25.14666667	2.742551889	0,39372	0.037460084
2279	PA2270_at	PA2270 /DEF=probable transcriptional regulator /FUN	-9.125031032	-98.18833333	10.7603287	0,49708	0.037460084
3593	PA3589_at	PA3589 /DEF=probable acyl-CoA thiolase /FUNCTION	-9.111336996	-19.34666667	2.123361991	0,46971	0.037460084
4356	PA4360_at	PA4360 /DEF=hypothetical protein /FUNCTION=Hypo	-9.060493676	-499.2633333	55.10332562	0,31610	0.037460084

1969	PA1959_bacA_at	PA1959 /GENE=bacA /DEF=bacitracin resistance prot	-9.034759432	-23.93666667	2.649397236	0,49533	0.037460084
2926	PA2921_at	PA2921 /DEF=probable transcriptional regulator /FUN	-9.018204841	-53.93166667	5.980310674	0,42471	0.037460084
4109	PA4107_at	PA4107 /DEF=hypothetical protein /FUNCTION=Hypo	-9.01603933	-72.60166667	8.052501105	0,33701	0.037460084
4840	PA4845_dipZ_at	PA4845 /GENE=dipZ /DEF=thiol:disulfide interchange	-9.013762741	-30.16	3.345994438	0,49014	0.037460084
4858	PA4863_at	PA4863 /DEF=hypothetical protein /FUNCTION=Hypo	-9.005752904	-86.37333333	9.590906419	0,49569	0.037460084
3913	PA3909_at	PA3909 /DEF=hypothetical protein /FUNCTION=Hypo	-8.980597123	-67.28333333	7.492077911	0,37982	0.037460084
2295	PA2286_at	PA2286 /DEF=hypothetical protein /FUNCTION=Meml	-8.949683116	-68.43333333	7.646453226	0,31658	0.037460084
2331	PA2324_at	PA2324 /DEF=hypothetical protein /FUNCTION=Putat	-8.932636371	-27.68166667	3.098935803	0,36617	0.037460084
207	PA0192_at	PA0192 /DEF=probable TonB-dependent receptor /FU	-8.92927189	-43.68166667	4.891962884	0,44825	0.037460084
325	PA0310_at	PA0310 /DEF=hypothetical protein /FUNCTION=Hypo	-8.90200264	-39.28333333	4.412864714	0,49576	0.037460084
1620	PA1606_at	PA1606 /DEF=hypothetical protein /FUNCTION=Hypo	-8.899471958	-79.93	8.981431749	0,36856	0.037460084
4896	PA4901_mdIC_a	PA4901 /GENE=mdIC /DEF=benzoylformate decarbox	-8.886003571	-15.58	1.753319124	0,49350	0.037460084
4839	PA4844_at	PA4844 /DEF=probable chemotaxis transducer /FUNC	-8.87891063	-122.8866667	13.84028647	0,20231	0.037460084
4780	PA4784_at	PA4784 /DEF=probable transcriptional regulator /FUN	-8.853706233	-158.4283333	17.89401288	0,21838	0.037460084
4868	PA4873_at	PA4873 /DEF=probable heat-shock protein /FUNCTION	-8.829786964	-59.86	6.779325508	0,46121	0.037460084
2343	PA2336_at	PA2336 /DEF=hypothetical protein /FUNCTION=Hypo	-8.818553156	-86.92333333	9.856870146	0,23731	0.037460084
4785	PA4789_at	PA4789 /DEF=conserved hypothetical protein /FUNCT	-8.817632247	-75.68	8.582802943	0,49901	0.037460084
4106	PA4104_at	PA4104 /DEF=conserved hypothetical protein /FUNCT	-8.799708579	-61.97	7.042278667	0,35390	0.037460084
4228	PA4231_pchA_at	PA4231 /GENE=pchA /DEF=salicylate biosynthesis is	-8.767771505	-191.1833333	21.80523674	0,34608	0.037460084
4394	PA4398_at	PA4398 /DEF=probable two-component sensor /FUNC	-8.742309642	-75.28833333	8.611949979	0,34785	0.037460084
4906	PA4911_at	PA4911 /DEF=probable permease of ABC branched-c	-8.715205224	-46.15333333	5.295725361	0,37608	0.037460084
4218	PA4221_fptA_at	PA4221 /GENE=fptA /DEF=Fe(III)-pyochelin receptor	-8.677350618	-671.665	77.40438638	0,25699	0.037460084
2333	PA2326_at	PA2326 /DEF=hypothetical protein /FUNCTION=Putat	-8.670157852	-33.36833333	3.848641963	0,40470	0.037460084
450	PA0435_at	PA0435 /DEF=hypothetical protein /FUNCTION=Hypo	-8.669117073	-83.23666667	9.601516044	0,36430	0.037460084
2523	PA2517_xylY_at	PA2517 /GENE=xylY /DEF=toluate 1,2-dioxygenase b	-8.658719605	-46.20333333	5.336046834	0,34036	0.037460084
3467	PA3463_at	PA3463 /DEF=conserved hypothetical protein /FUNCT	-8.638754049	-267.9116667	31.01276702	0,29641	0.037460084
2793	PA2788_at	PA2788 /DEF=probable chemotaxis transducer /FUNC	-8.632055099	-83.695	9.695837091	0,26045	0.037460084
2372	PA2365_at	PA2365 /DEF=conserved hypothetical protein /FUNCT	-8.588101993	-35.87166667	4.176902731	0,41877	0.037460084
188	PA0173_at	PA0173 /DEF=probable methylesterase /FUNCTION=	-8.57445638	-45.65333333	5.324341429	0,40019	0.037460084
803	PA0788_at	PA0788 /DEF=hypothetical protein /FUNCTION=Hypo	-8.523541285	-62.94333333	7.384645798	0,33980	0.037460084
2925	PA2920_at	PA2920 /DEF=probable chemotaxis transducer /FUNC	-8.511957697	-46.895	5.509308395	0,35162	0.037460084
4588	PA4592_at	PA4592 /DEF=hypothetical protein /FUNCTION=Hypo	-8.499943586	-58.83166667	6.921418486	0,47739	0.037460084
41	PA0026_at	PA0026 /DEF=hypothetical protein /FUNCTION=Hypo	-8.495919109	-23.06333333	2.714636643	0,49386	0.037460084
349	PA0334_at	PA0334 /DEF=probable MFS transporter /FUNCTION=	-8.442952286	-101.9883333	12.07970031	0,43778	0.037460084
223	PA0208_mdca_a	PA0208 /GENE=mdcA /DEF=malonate decarboxylase	-8.435129672	-56.54166667	6.70311766	0,42611	0.037460084
4890	PA4895_at	PA4895 /DEF=probable transmembrane sensor /FUNC	-8.419308874	-29.68333333	3.525625889	0,39570	0.037460084

4041	PA4039_at	PA4039 /DEF=hypothetical protein /FUNCTION=Hypo	-8.388962519	-20.23666667	2.412296708	0,43272	0.037460084
4829	PA4834_at	PA4834 /DEF=hypothetical protein /FUNCTION=Hypo	-8.381312861	-74.48333333	8.88683367	0,20841	0.037460084
192	PA0177_at	PA0177 /DEF=probable purine-binding chemotaxis prc	-8.370480482	-35.61	4.254236071	0,30090	0.037460084
4032	PA4030_at	PA4030 /DEF=conserved hypothetical protein /FUNCT	-8.360231375	-81.375	9.733582284	0,40637	0.037460084
4832	PA4837_at	PA4837 /DEF=probable outer membrane protein /FUN	-8.343154794	-42.115	5.047850728	0,42369	0.037460084
4327	PA4331_at	PA4331 /DEF=probable ferredoxin reductase /FUNCTI	-8.31253778	-19.665	2.365703534	0,49809	0.037460084
233	PA0218_at	PA0218 /DEF=probable transcriptional regulator /FUNI	-8.304795416	-21.405	2.577426526	0,46110	0.037460084
226	PA0211_mdcD_g	PA0211 /GENE=mdcD /DEF=malonate decarboxylase	-8.261946391	-50.43166667	6.104090281	0,39764	0.037460084
4877	PA4882_at	PA4882 /DEF=hypothetical protein /FUNCTION=Hypo	-8.25627352	-62.01333333	7.511056069	0,35434	0.037460084
2934	PA2929_at	PA2929 /DEF=hypothetical protein /FUNCTION=Hypo	-8.242320717	-45.16	5.479039405	0,38948	0.037460084
2351	PA2344_mtlZ_at	PA2344 /GENE=mtlZ /DEF=fructokinase /FUNCTION=	-8.229808533	-79.80666667	9.69726894	0,41995	0.037460084
4852	PA4857_at	PA4857 /DEF=hypothetical protein /FUNCTION=Hypo	-8.195921862	-21.16666667	2.58258522	0,42377	0.037460084
2075	PA2066_at	PA2066 /DEF=hypothetical protein /FUNCTION=Hypo	-8.19586168	-125.8883333	15.35998755	0,29293	0.037460084
2356	PA2349_at	PA2349 /DEF=conserved hypothetical protein /FUNCT	-8.186832666	-22.985	2.807557078	0,49242	0.037460084
2284	PA2275_at	PA2275 /DEF=probable alcohol dehydrogenase (Zn-d	-8.184712993	-46.62333333	5.696391965	0,36705	0.037460084
1481	PA1466_at	PA1466 /DEF=hypothetical protein /FUNCTION=Hypo	-8.128746515	-52.31666667	6.436006655	0,49716	0.037460084
4170	PA4168_at	PA4168 /DEF=probable TonB-dependent receptor /FU	-8.126377106	-52.17666667	6.420655353	0,39671	0.037460084
5389	PA5395_at	PA5395 /DEF=conserved hypothetical protein /FUNCT	-8.120482799	-27.59166667	3.39778648	0,49112	0.037460084
2129	PA2120_at	PA2120 /DEF=hypothetical protein /FUNCTION=Hypo	-8.1182841	-25.69833333	3.1654883	0,41270	0.037460084
2867	PA2862_lipA_at	PA2862 /GENE=lipA /DEF=lactonizing lipase precurs	-8.115025897	-434.0466667	53.48678762	0,07992	0.037460084
4634	PA4638_at	PA4638 /DEF=hypothetical protein /FUNCTION=Hypo	-8.111184037	-49.55166667	6.109054663	0,39529	0.037460084
4821	PA4826_at	PA4826 /DEF=hypothetical protein /FUNCTION=Hypo	-8.101352879	-55.09833333	6.801127436	0,29458	0.037460084
2341	PA2334_at	PA2334 /DEF=probable transcriptional regulator /FUNI	-8.062935026	-40.55166667	5.029392713	0,47734	0.037460084
4910	PA4915_at	PA4915 /DEF=probable chemotaxis transducer /FUNC	-8.033281468	-224.24	27.91387317	0,32185	0.037460084
1317	PA1302_at	PA1302 /DEF=probable heme utilization protein precu	-8.029708644	-33.34	4.152080913	0,42865	0.037460084
2108	PA2099_at	PA2099 /DEF=probable short-chain dehydrogenase /F	-8.01798798	-60.96333333	7.603320619	0,34565	0.037460084
2373	PA2366_at	PA2366 /DEF=conserved hypothetical protein /FUNCT	-8.004280266	-69.54166667	8.688059932	0,29628	0.037460084
2094	PA2085_at	PA2085 /DEF=probable ring-hydroxylating dioxygenas	-8.00137708	-37.81833333	4.726478074	0,36896	0.037460084
2924	PA2919_at	PA2919 /DEF=hypothetical protein /FUNCTION=Hypo	-7.978958956	-19.065	2.389409459	0,43338	0.037460084
2510	PA2504_at	PA2504 /DEF=hypothetical protein /FUNCTION=Hypo	-7.967368048	-125.1216667	15.70426594	0,32834	0.037460084
2313	PA2305_at	PA2305 /DEF=probable non-ribosomal peptide synthe	-7.905587643	-89.00833333	11.25891425	0,23266	0.037460084
1037	PA1022_at	PA1022 /DEF=probable acyl-CoA dehydrogenase /FU	-7.89435844	-39.15666667	4.960082186	0,46016	0.037460084
2105	PA2096_at	PA2096 /DEF=probable transcriptional regulator /FUNI	-7.862622609	-63.72166667	8.104378124	0,34885	0.037460084
2345	PA2338_at	PA2338 /DEF=probable binding protein component of	-7.848877922	-61.865	7.882018375	0,30846	0.037460084
2358	PA2351_at	PA2351 /DEF=probable permease of ABC transporter	-7.845029176	-24.66333333	3.143816649	0,49571	0.037460084
361	PA0346_at	PA0346 /DEF=hypothetical protein /FUNCTION=Hypo	-7.830037811	-52.36333333	6.687494314	0,46773	0.037460084

3446	PA3442_at	PA3442 /DEF=probable ATP-binding component of A	-7.741125582	-48.23166667	6.230575406	0,48275	0.037460084
4321	PA4325_at	PA4325 /DEF=hypothetical protein /FUNCTION=Hypo	-7.70003814	-285.48	37.07514103	0,31080	0.037460084
2101	PA2092_at	PA2092 /DEF=probable MFS transporter /FUNCTION=	-7.690805595	-38.925	5.061238321	0,34107	0.037460084
4155	PA4153_at	PA4153 /DEF=2,3-butanediol dehydrogenase /FUNCT	-7.644302961	-30.23666667	3.955451114	0,47636	0.037460084
466	PA0451_at	PA0451 /DEF=conserved hypothetical protein /FUNCT	-7.644000289	-53.50833333	7.000043343	0,42931	0.037460084
2914	PA2909_i_at	PA2909 /DEF=hypothetical protein /FUNCTION=Biosy	-7.611618513	-77.87333333	10.2308508	0,42585	0.037460084
1928	PA1916_at	PA1916 /DEF=probable amino acid permease /FUNCT	-7.589684127	-18.02666667	2.375153744	0,48520	0.037460084
2660	PA2654_at	PA2654 /DEF=probable chemotaxis transducer /FUNC	-7.561036052	-138.7566667	18.35154147	0,36751	0.037460084
4815	PA4820_at	PA4820 /DEF=hypothetical protein /FUNCTION=Hypo	-7.522446915	-19.87166667	2.641649305	0,42340	0.037460084
22	PA0007_at	PA0007 /DEF=hypothetical protein /FUNCTION=Hypo	-7.517764447	-43.56666667	5.795162508	0,46412	0.037460084
4644	PA4648_at	PA4648 /DEF=hypothetical protein /FUNCTION=Hypo	-7.513401824	-38.34666667	5.103768914	0,44543	0.037460084
4897	PA4902_at	PA4902 /DEF=probable transcriptional regulator /FUNI	-7.509404377	-63.42166667	8.445632102	0,40602	0.037460084
4581	PA4585_rtcA_at	PA4585 /GENE=rtcA /DEF=RNA 3'-terminal phosphat	-7.505877503	-44.88166667	5.979536256	0,46307	0.037460084
2500	PA2494_mexF_a	PA2494 /GENE=mexF /DEF=RND multidrug efflux trar	-7.492771488	-24.90833333	3.324315091	0,41807	0.037460084
4050	PA4048_at	PA4048 /DEF=hypothetical protein /FUNCTION=Hypo	-7.488181791	-26.10666667	3.486382595	0,44505	0.037460084
2927	PA2922_at	PA2922 /DEF=probable hydrolase /FUNCTION=Putati	-7.485617375	-95.06666667	12.69990996	0,23859	0.037460084
150	PA0135_at	PA0135 /DEF=hypothetical protein /FUNCTION=Hypo	-7.478308376	-29.72	3.9741608	0,36739	0.037460084
2370	PA2363_at	PA2363 /DEF=hypothetical protein /FUNCTION=Hypo	-7.477949298	-51.02833333	6.823840508	0,46801	0.037460084
3573	PA3569_mmsB_i	PA3569 /GENE=mmsB /DEF=3-hydroxyisobutyrate de	-7.459895331	-658.0883333	88.21683203	0,16813	0.037460084
123	PA0108_colII_at	PA0108 /GENE=colII /DEF=cytochrome c oxidase, sul	-7.446576757	-927.955	124.6149782	0,06972	0.037460084
236	PA0221_at	PA0221 /DEF=probable aminotransferase /FUNCTION	-7.44133796	-39.94333333	5.367762296	0,37569	0.037460084
2528	PA2522_czcC_at	PA2522 /GENE=czcC /DEF=outer membrane protein i	-7.435582742	-18.26833333	2.456879839	0,49716	0.037460084
2280	PA2271_i_at	PA2271 /DEF=probable acetyltransferase /FUNCTION	-7.421697184	-71.995	9.700611359	0,46838	0.037460084
122	PA0107_at	PA0107 /DEF=conserved hypothetical protein /FUNCT	-7.41945843	-295.91	39.88296488	0,15926	0.037460084
4791	PA4795_at	PA4795 /DEF=hypothetical protein /FUNCTION=Hypo	-7.376929573	-71.28166667	9.662782593	0,48039	0.037460084
772	PA0757_at	PA0757 /DEF=probable two-component sensor /FUNC	-7.360576264	-67.7	9.19764942	0,43788	0.037460084
2335	PA2328_at	PA2328 /DEF=hypothetical protein /FUNCTION=Hypo	-7.356833723	-52.755	7.170883832	0,43828	0.037460084
865	PA0850_at	PA0850 /DEF=hypothetical protein /FUNCTION=Hypo	-7.350158924	-38.63166667	5.255895425	0,44838	0.037460084
2886	PA2881_at	PA2881 /DEF=probable two-component response regu	-7.343126356	-44.79	6.099581817	0,35433	0.037460084
4373	PA4377_at	PA4377 /DEF=hypothetical protein /FUNCTION=Hypo	-7.338236463	-619.0483333	84.35927849	0,21881	0.037460084
2312	PA2304_at	PA2304 /DEF=hypothetical protein /FUNCTION=Hypo	-7.338121405	-56.58833333	7.711555889	0,41963	0.037460084
3436	PA3431_at	PA3431 /DEF=conserved hypothetical protein /FUNCT	-7.337173882	-41.79666667	5.696562101	0,40076	0.037460084
5214	PA5219_at	PA5219 /DEF=hypothetical protein /FUNCTION=Hypo	-7.317019299	-22.64166667	3.094383893	0,47661	0.037460084
2904	PA2899_at	PA2899 /DEF=probable transcriptional regulator /FUNI	-7.289657875	-100.3383333	13.76447771	0,45929	0.037460084
4216	PA4219_at	PA4219 /DEF=hypothetical protein /FUNCTION=Hypo	-7.282620774	-118.55	16.27848046	0,41862	0.037460084
4795	PA4800_at	PA4800 /DEF=hypothetical protein /FUNCTION=Hypo	-7.230010178	-32.18666667	4.451814849	0,44490	0.037460084

1708	PA1694_pscQ_a	PA1694 /GENE=pscQ /DEF=translocation protein in ty	-7.216035083	-97.17166667	13.46607459	0,32252	0.037460084
5404	PA5410_at	PA5410 /DEF=probable ring hydroxylating dioxygenas	-7.189660528	-146.3183333	20.35121585	0,21629	0.037460084
4771	PA4775_at	PA4775 /DEF=hypothetical protein /FUNCTION=Hypo	-7.172026714	-44.88	6.257645404	0,42028	0.037460084
3910	PA3906_at	PA3906 /DEF=hypothetical protein /FUNCTION=Hypo	-7.133641802	-55.12166667	7.727002307	0,31591	0.037460084
225	PA0210_mdcC_ε	PA0210 /GENE=mdcC /DEF=malonate decarboxylase	-7.095237501	-61.735	8.700906769	0,28053	0.037460084
4784	PA4788_at	PA4788 /DEF=hypothetical protein /FUNCTION=Hypo	-7.092720416	-137.0916667	19.32850283	0,30255	0.037460084
2080	PA2071_fusA2_ε	PA2071 /GENE=fusA2 /DEF=elongation factor G /FUN	-7.090606532	-68.465	9.655732509	0,36823	0.037460084
201	PA0186_at	PA0186 /DEF=probable binding protein component of	-7.074830844	-21.72	3.070038066	0,43072	0.037460084
3423	PA3418_ldh_at	PA3418 /GENE=ldh /DEF=leucine dehydrogenase /FU	-7.071588491	-212.6316667	30.06844458	0,33000	0.037460084
4813	PA4818_at	PA4818 /DEF=conserved hypothetical protein /FUNCT	-7.003275652	-76.96666667	10.99009528	0,36864	0.037460084
5175	PA5180_at	PA5180 /DEF=conserved hypothetical protein /FUNCT	-6.997247622	-71.10666667	10.16209094	0,42731	0.037460084
3875	PA3871_at	PA3871 /DEF=probable peptidyl-prolyl cis-trans isome	-6.988042372	-23.25833333	3.328304566	0,46409	0.037460084
4776	PA4780_at	PA4780 /DEF=conserved hypothetical protein /FUNCT	-6.97060847	-119.0333333	17.07646238	0,49221	0.037460084
165	PA0150_at	PA0150 /DEF=probable transmembrane sensor /FUNC	-6.968165558	-39.245	5.632041844	0,47666	0.037460084
3928	PA3924_at	PA3924 /DEF=probable medium-chain acyl-CoA ligase	-6.966655268	-63.84166667	9.163890592	0,36045	0.037460084
767	PA0752_at	PA0752 /DEF=conserved hypothetical protein /FUNCT	-6.944437652	-21.915	3.155763087	0,49236	0.037460084
2921	PA2916_at	PA2916 /DEF=hypothetical protein /FUNCTION=Hypo	-6.943196609	-100.3	14.44579574	0,28354	0.037460084
801	PA0786_at	PA0786 /DEF=probable transporter /FUNCTION=Mem	-6.918505959	-21.85666667	3.15915991	0,42843	0.037460084
5412	PA5418_soxA_at	PA5418 /GENE=soxA /DEF=sarcosine oxidase alpha :	-6.891529365	-82.605	11.98645404	0,43856	0.037460084
1984	PA1974_at	PA1974 /DEF=hypothetical protein /FUNCTION=Hypo	-6.86551891	-41.84333333	6.094708045	0,39669	0.037460084
5374	PA5380_at	PA5380 /DEF=probable transcriptional regulator /FUN	-6.848074528	-274.88	40.13975007	0,44784	0.037460084
5132	PA5137_at	PA5137 /DEF=hypothetical protein /FUNCTION=Hypo	-6.799790102	-53.69833333	7.897057487	0,44569	0.037460084
4351	PA4355_at	PA4355 /DEF=probable MFS transporter /FUNCTION=	-6.794358917	-69.35666667	10.20797805	0,46949	0.037460084
340	PA0325_at	PA0325 /DEF=probable permease of ABC transporter	-6.754450385	-33.07333333	4.896524728	0,40768	0.037460084
2107	PA2098_at	PA2098 /DEF=probable esterase/deacetylase /FUNCT	-6.720301733	-67.34333333	10.02087942	0,41452	0.037460084
3572	PA3568_at	PA3568 /DEF=probable acetyl-coa synthetase /FUNC	-6.709292309	-483.13	72.00908498	0,15684	0.037460084
4816	PA4821_at	PA4821 /DEF=probable transporter /FUNCTION=Tran	-6.70044535	-48.06166667	7.172906301	0,46586	0.037460084
4830	PA4835_at	PA4835 /DEF=hypothetical protein /FUNCTION=Mem	-6.693765664	-28.56333333	4.267154658	0,49091	0.037460084
1499	PA1484_at	PA1484 /DEF=probable transcriptional regulator /FUN	-6.662191146	-22.02833333	3.306469726	0,48444	0.037460084
3915	PA3911_at	PA3911 /DEF=conserved hypothetical protein /FUNCT	-6.651730824	-59.25833333	8.908708861	0,47818	0.037460084
1633	PA1619_at	PA1619 /DEF=probable transcriptional regulator /FUN	-6.644503674	-83.92166667	12.63023858	0,46904	0.037460084
4809	PA4814_fadH2_ε	PA4814 /GENE=fadH2 /DEF=2,4-dienoyl-CoA reducta	-6.638531975	-67.58166667	10.18021257	0,36779	0.037460084
4085	PA4083_at	PA4083 /DEF=probable pili assembly chaperone /FUN	-6.634167299	-23.29333333	3.511116359	0,49211	0.037460084
3884	PA3880_at	PA3880 /DEF=conserved hypothetical protein /FUNCT	-6.620185747	-89.885	13.5774136	0,44204	0.037460084
2097	PA2088_at	PA2088 /DEF=hypothetical protein /FUNCTION=Hypo	-6.579920944	-25.63	3.895183577	0,38409	0.037460084
4292	PA4296_at	PA4296 /DEF=probable two-component response regu	-6.562397943	-137.015	20.87880089	0,27657	0.037460084

244	PA0229_pcaT_at	PA0229 /GENE=pcaT /DEF=dicarboxylic acid transpor	-6.562290089	-20.85	3.177244486	0,45811	0.037460084
121	PA0106_coxA_at	PA0106 /GENE=coxA /DEF=cytochrome c oxidase, su	-6.525260279	-433.6466667	66.45660834	0,10792	0.037460084
2382	PA2375_i_at	PA2375 /DEF=hypothetical protein /FUNCTION=Hypo	-6.518942782	-72.32	11.0938234	0,43125	0.037460084
4465	PA4469_at	PA4469 /DEF=hypothetical protein /FUNCTION=Hypo	-6.483857738	-72.34666667	11.15796638	0,44925	0.037460084
1964	PA1954_at	PA1954 /DEF=hypothetical protein /FUNCTION=Hypo	-6.477969737	-33.43833333	5.161853897	0,37530	0.037460084
153	PA0138_at	PA0138 /DEF=probable permease of ABC transporter	-6.460699064	-48.13	7.449658237	0,35884	0.037460084
4853	PA4858_at	PA4858 /DEF=conserved hypothetical protein /FUNCT	-6.456543396	-14.895	2.306961959	0,49966	0.037460084
4360	PA4364_at	PA4364 /DEF=hypothetical protein /FUNCTION=Hypo	-6.451630845	-28.22833333	4.375379499	0,43716	0.037460084
379	PA0364_at	PA0364 /DEF=probable oxidoreductase /FUNCTION= 	-6.451187016	-22.42	3.475329415	0,44647	0.037460084
5462	PA5468_at	PA5468 /DEF=probable citrate transporter /FUNCTION	-6.443666023	-42.87	6.653044998	0,31988	0.037460084
2294	PA2285_at	PA2285 /DEF=hypothetical protein /FUNCTION=Hypo	-6.441507066	-71.95833333	11.17104004	0,32741	0.037460084
5353	PA5359_at	PA5359 /DEF=hypothetical protein /FUNCTION=Hypo	-6.440596048	-132.8533333	20.62749043	0,40332	0.037460084
1980	PA1970_at	PA1970 /DEF=hypothetical protein /FUNCTION=Hypo	-6.432380384	-19.95166667	3.10175479	0,49064	0.037460084
2941	PA2936_at	PA2936 /DEF=hypothetical protein /FUNCTION=Hypo	-6.417497314	-33.04333333	5.148943851	0,34928	0.037460084
4879	PA4884_at	PA4884 /DEF=hypothetical protein /FUNCTION=Hypo	-6.391212374	-54.26666667	8.490825135	0,47146	0.037460084
4881	PA4886_at	PA4886 /DEF=probable two-component sensor /FUNC	-6.354932651	-24.98666667	3.931853891	0,45440	0.037460084
362	PA0347_glpQ_at	PA0347 /GENE=glpQ /DEF=glycerophosphoryl diester	-6.321889988	-49.57833333	7.842327757	0,36725	0.037460084
2877	PA2872_at	PA2872 /DEF=hypothetical protein /FUNCTION=Hypo	-6.320603311	-85.06666667	13.45863084	0,42585	0.037460084
2353	PA2346_at	PA2346 /DEF=conserved hypothetical protein /FUNCT	-6.318974808	-29.09833333	4.604913648	0,40299	0.037460084
4463	PA4467_at	PA4467 /DEF=hypothetical protein /FUNCTION=Hypo	-6.30438052	-33.18666667	5.264064655	0,44064	0.037460084
4029	PA4027_at	PA4027 /DEF=hypothetical protein /FUNCTION=Hypo	-6.296626008	-46.78833333	7.430699119	0,41324	0.037460084
2355	PA2348_at	PA2348 /DEF=conserved hypothetical protein /FUNCT	-6.293615095	-47.78333333	7.592350757	0,33696	0.037460084
2329	PA2322_at	PA2322 /DEF=gluconate permease /FUNCTION=Tran	-6.280595299	-49.22666667	7.837898212	0,40607	0.037460084
241	PA0226_at	PA0226 /DEF=probable CoA transferase, subunit A /F	-6.259236148	-148.815	23.7752653	0,23509	0.037460084
4908	PA4913_at	PA4913 /DEF=probable binding protein component of	-6.204697498	-85.80166667	13.82850118	0,20937	0.037460084
3095	PA3090_at	PA3090 /DEF=hypothetical protein /FUNCTION=Hypo	-6.20194262	-45.80833333	7.386126596	0,43281	0.037460084
2102	PA2093_at	PA2093 /DEF=probable sigma-70 factor, ECF subfami	-6.18654025	-29.34666667	4.743631413	0,41377	0.037460084
4817	PA4822_at	PA4822 /DEF=hypothetical protein /FUNCTION=Hypo	-6.185612419	-44.71666667	7.229141375	0,35539	0.037460084
5215	PA5220_at	PA5220 /DEF=hypothetical protein /FUNCTION=Hypo	-6.177962614	-31.34166667	5.073139581	0,49329	0.037460084
3096	PA3091_at	PA3091 /DEF=hypothetical protein /FUNCTION=Hypo	-6.15393341	-25.14166667	4.085462905	0,47821	0.037460084
4587	PA4591_at	PA4591 /DEF=hypothetical protein /FUNCTION=Hypo	-6.153042464	-114.8716667	18.66908401	0,25326	0.037460084
2104	PA2095_at	PA2095 /DEF=hypothetical protein /FUNCTION=Hypo	-6.15189165	-19.18666667	3.118823893	0,46486	0.037460084
3455	PA3451_at	PA3451 /DEF=hypothetical protein /FUNCTION=Hypo	-6.114095858	-40.72833333	6.661382856	0,29106	0.037460084
4904	PA4909_at	PA4909 /DEF=probable ATP-binding component of AE	-6.095778687	-39.96833333	6.556723167	0,31608	0.037460084
4225	PA4228_pchD_a	PA4228 /GENE=pchD /DEF=pyochelin biosynthesis pr	-6.095130532	-306.59	50.30080954	0,26614	0.037460084
4357	PA4361_at	PA4361 /DEF=probable oxidoreductase /FUNCTION= 	-6.093054553	-65.44166667	10.74037104	0,45281	0.037460084

2314	PA2306_at	PA2306 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical protein	-6.04607454	-31.79333333	5.25850833	0,36926	0.037460084
2302	PA2294_at	PA2294 /DEF=probable ATP-binding component of ATP synthase	-6.01867127	-42.87666667	7.12394227	0,44434	0.037460084
2317	PA2309_at	PA2309 /DEF=hypothetical protein /FUNCTION=Hypothetical protein	-5.9733582	-44.465	7.443886422	0,33654	0.037460084
4466	PA4470_fumC1_	PA4470 /GENE=fumC1 /DEF=fumarate hydratase /FUNCTION=Hypothetical protein	-5.972950037	-67.44333333	11.29146116	0,46486	0.037460084
3453	PA3449_at	PA3449 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical protein	-5.972942255	-19.69666667	3.297648935	0,46253	0.037460084
4797	PA4802_at	PA4802 /DEF=hypothetical protein /FUNCTION=Hypothetical protein	-5.951746246	-74.36	12.49381222	0,39212	0.037460084
2332	PA2325_at	PA2325 /DEF=hypothetical protein /FUNCTION=Putative protein	-5.945052536	-46.82333333	7.876016747	0,39227	0.037460084
4359	PA4363_iciA_at	PA4363 /GENE=iciA /DEF=inhibitor of chromosome inactivation	-5.941127976	-23.46	3.948745103	0,45573	0.037460084
2525	PA2519_xylS_at	PA2519 /GENE=xylS /DEF=transcriptional regulator XylS	-5.936552593	-59.87666667	10.0861006	0,39106	0.037460084
3430	PA3425_at	PA3425 /DEF=hypothetical protein /FUNCTION=Hypothetical protein	-5.893298842	-51.04	8.660684171	0,48118	0.037460084
4831	PA4836_at	PA4836 /DEF=hypothetical protein /FUNCTION=Hypothetical protein	-5.883116914	-42.64666667	7.248991868	0,33987	0.037460084
380	PA0365_at	PA0365 /DEF=hypothetical protein /FUNCTION=Hypothetical protein	-5.871148982	-60.27	10.26545233	0,42932	0.037460084
4320	PA4324_at	PA4324 /DEF=hypothetical protein /FUNCTION=Hypothetical protein	-5.852216745	-52.95	9.047853541	0,39736	0.037460084
4380	PA4384_at	PA4384 /DEF=hypothetical protein /FUNCTION=Hypothetical protein	-5.830425888	-63.21666667	10.84254699	0,48250	0.037460084
4042	PA4040_at	PA4040 /DEF=hypothetical protein /FUNCTION=Hypothetical protein	-5.820398774	-49.61	8.523470972	0,39151	0.037460084
2520	PA2514_antC_at	PA2514 /GENE=antC /DEF=anthranilate dioxygenase	-5.812942599	-182.2483333	31.35216463	0,10885	0.037460084
1888	PA1874_at	PA1874 /DEF=hypothetical protein /FUNCTION=Hypothetical protein	-5.807331682	-50.64833333	8.721446632	0,42486	0.037460084
3483	PA3479_rhlA_at	PA3479 /GENE=rhlA /DEF=rhamnosyltransferase chain A	-5.804373366	-24.56166667	4.231579383	0,41971	0.037460084
1438	PA1423_at	PA1423 /DEF=probable chemotaxis transducer /FUNCTION=Hypothetical protein	-5.750300113	-17.93833333	3.119547325	0,46654	0.037460084
2078	PA2069_at	PA2069 /DEF=probable carbamoyl transferase /FUNCTION=Hypothetical protein	-5.741447128	-41.45833333	7.220885677	0,37048	0.037460084
4876	PA4881_at	PA4881 /DEF=hypothetical protein /FUNCTION=Hypothetical protein	-5.740764394	-63.43666667	11.05021254	0,25932	0.037460084
3072	PA3067_at	PA3067 /DEF=probable transcriptional regulator /FUNCTION=Hypothetical protein	-5.717854195	-81.28666667	14.21628882	0,33542	0.037460084
2086	PA2077_at	PA2077 /DEF=hypothetical protein /FUNCTION=Hypothetical protein	-5.654683157	-26.54	4.693454835	0,49614	0.037460084
4892	PA4897_at	PA4897 /DEF=hypothetical protein /FUNCTION=Hypothetical protein	-5.648627958	-31.91333333	5.649749563	0,44178	0.037460084
3422	PA3417_at	PA3417 /DEF=probable pyruvate dehydrogenase E1 component	-5.63800365	-82.335	14.60357338	0,32977	0.037460084
1706	PA1692_at	PA1692 /DEF=probable translocation protein in type III secretion system	-5.63083611	-115.5883333	20.52773888	0,27318	0.037460084
4065	PA4063_at	PA4063 /DEF=hypothetical protein /FUNCTION=Hypothetical protein	-5.618019832	-58.8	10.46632119	0,39740	0.037460084
4782	PA4786_at	PA4786 /DEF=probable short-chain dehydrogenase /FUNCTION=Hypothetical protein	-5.58437987	-33.84166667	6.060058136	0,49785	0.037460084
883	PA0868_at	PA0868 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical protein	-5.557289845	-59.18166667	10.64937556	0,46246	0.037460084
1917	PA1905_s_at	PA1905 /DEF=probable pyridoxamine 5'-phosphate oxidase	-5.494189062	-62.27833333	11.33530948	0,38422	0.037460084
400	PA0385_at	PA0385 /DEF=hypothetical protein /FUNCTION=Hypothetical protein	-5.486345683	-39.12666667	7.131644436	0,35984	0.037460084
4171	PA4169_at	PA4169 /DEF=conserved hypothetical protein /FUNCTION=Hypothetical protein	-5.485536299	-27.79333333	5.066657446	0,46814	0.037460084
3420	PA3415_at	PA3415 /DEF=probable dihydrolipoamide acetyltransferase	-5.475910373	-55.90833333	10.20987005	0,44725	0.037460084
228	PA0213_at	PA0213 /DEF=hypothetical protein /FUNCTION=Carbamoyl transferase	-5.470579585	-34.32	6.273558307	0,42281	0.037460084
4148	PA4146_at	PA4146 /DEF=hypothetical protein /FUNCTION=Hypothetical protein	-5.459943807	-35.16166667	6.439931968	0,43339	0.037460084
2348	PA2341_at	PA2341 /DEF=probable ATP-binding component of ATP synthase	-5.458467341	-31.76166667	5.81878844	0,46848	0.037460084

796	PA0781_at	PA0781 /DEF=hypothetical protein /FUNCTION=Hypo	-5.42917732	-42.32	7.79491947	0,42035	0.037460084
2307	PA2299_at	PA2299 /DEF=probable transcriptional regulator /FUN	-5.426942154	-30.41666667	5.604752327	0,47111	0.037460084
169	PA0154_pcaG_a	PA0154 /GENE=pcaG /DEF=protocatechuate 3,4-diox	-5.406121486	-212.1383333	39.2403933	0,27603	0.037460084
3727	PA3723_at	PA3723 /DEF=probable FMN oxidoreductase /FUNCT	-5.390000613	-443.2116667	82.22850023	0,33337	0.037460084
4226	PA4229_pchC_a	PA4229 /GENE=pchC /DEF=pyochelin biosynthetic pr	-5.379635518	-181.36	33.7123211	0,32573	0.037460084
4865	PA4870_at	PA4870 /DEF=conserved hypothetical protein /FUNCT	-5.374122268	-54.26333333	10.09715273	0,46563	0.037460084
1777	PA1763_at	PA1763 /DEF=hypothetical protein /FUNCTION=Hypo	-5.344051535	-16.63666667	3.113118681	0,46489	0.037460084
4191	PA4189_at	PA4189 /DEF=probable aldehyde dehydrogenase /FU	-5.317747641	-40.9	7.691226203	0,44296	0.037460084
4219	PA4222_at	PA4222 /DEF=probable ATP-binding component of AE	-5.310880007	-139.7766667	26.31892765	0,39391	0.037460084
2301	PA2293_at	PA2293 /DEF=hypothetical protein /FUNCTION=Hypo	-5.310535533	-56.06833333	10.55794335	0,41384	0.037460084
1281	PA1266_at	PA1266 /DEF=probable oxidoreductase /FUNCTION= 	-5.299424043	-34.16666667	6.447241509	0,47274	0.037460084
4043	PA4041_at	PA4041 /DEF=hypothetical protein /FUNCTION=Putat	-5.294772013	-48.72666667	9.202788438	0,33494	0.037460084
2283	PA2274_at	PA2274 /DEF=hypothetical protein /FUNCTION=Hypo	-5.292053928	-71.31333333	13.47554925	0,25018	0.037460084
1883	PA1869_at	PA1869 /DEF=probable acyl carrier protein /FUNCTIO	-5.23899386	-31.89833333	6.088637281	0,42126	0.037460084
1190	PA1175_napD_a	PA1175 /GENE=napD /DEF=NapD protein of periplasr	-5.226168632	-57.74666667	11.04952227	0,35792	0.037460084
256	PA0241_at	PA0241 /DEF=probable MFS transporter /FUNCTION=	-5.214625796	-90.54	17.3627032	0,28538	0.037460084
4393	PA4397_panE_a	PA4397 /GENE=panE /DEF=keto-pantoate reductase /	-5.206215251	-44.34	8.51674352	0,43453	0.037460084
2866	PA2861_ligT_at	PA2861 /GENE=ligT /DEF=2'-5' RNA ligase /FUNCTIC	-5.19677055	-16.285	3.133676933	0,45693	0.037460084
5208	PA5213_gcvP1_i	PA5213 /GENE=gcvP1 /DEF=glycine cleavage system	-5.18806697	-35.15166667	6.77548437	0,48699	0.037460084
4898	PA4903_at	PA4903 /DEF=probable MFS transporter /FUNCTION=	-5.172913508	-26.025	5.031013946	0,48927	0.037460084
2296	PA2287_at	PA2287 /DEF=hypothetical protein /FUNCTION=Hypo	-5.164077898	-44.66166667	8.64852691	0,38859	0.037460084
2070	PA2061_at	PA2061 /DEF=probable ATP-binding component of AE	-5.126964892	-15.88666667	3.098649396	0,46683	0.037460084
4387	PA4391_at	PA4391 /DEF=hypothetical protein /FUNCTION=Hypo	-5.122090004	-43.005	8.395986788	0,42198	0.037460084
1868	PA1854_at	PA1854 /DEF=conserved hypothetical protein /FUNCT	-5.121094683	-37.95666667	7.411826771	0,36385	0.037460084
1937	PA1925_at	PA1925 /DEF=hypothetical protein /FUNCTION=Hypo	-5.111002022	-17.205	3.3662675	0,48529	0.037460084
3356	PA3351_at	PA3351 /DEF=hypothetical protein /FUNCTION=Hypo	-5.071544055	-713.7866667	140.7434617	0,36974	0.037460084
2515	PA2509_catB_at	PA2509 /GENE=catB /DEF=muconate cycloisomerase	-5.044187374	-49.75666667	9.864159077	0,35548	0.037460084
206	PA0191_at	PA0191 /DEF=probable transcriptional regulator /FUN	-4.95020867	-26.54666667	5.362736894	0,43745	0.037460084
2948	PA2943_at	PA2943 /DEF=phospho-2-dehydro-3-deoxyheptonate :	-4.946753039	-67.07	13.5583886	0,45189	0.037460084
128	PA0113_at	PA0113 /DEF=probable cytochrome c oxidase assembl	-4.909037542	-107.825	21.96459063	0,28813	0.037460084
2412	PA2405_at	PA2405 /DEF=hypothetical protein /FUNCTION=Hypo	-4.895169509	-35.585	7.269411189	0,39731	0.037460084
2380	PA2373_at	PA2373 /DEF=conserved hypothetical protein /FUNCT	-4.884749842	-51.20333333	10.48228364	0,39706	0.037460084
253	PA0238_at	PA0238 /DEF=hypothetical protein /FUNCTION=Hypo	-4.880132273	-216.3216667	44.3270089	0,13646	0.037460084
2414	PA2407_at	PA2407 /DEF=probable adhesion protein /FUNCTION=	-4.873929423	-48.24833333	9.899267952	0,47005	0.037460084
179	PA0164_at	PA0164 /DEF=probable gamma-glutamyltranspeptidas	-4.867718993	-30.79833333	6.327056549	0,42885	0.037460084
2318	PA2310_at	PA2310 /DEF=hypothetical protein /FUNCTION=Putat	-4.854092295	-29.15833333	6.006958987	0,45133	0.037460084

4377	PA4381_at	PA4381 /DEF=probable two-component response regu	-4.842205974	-61.78833333	12.76036866	0,46541	0.037460084
4371	PA4375_at	PA4375 /DEF=probable RND efflux transporter /FUNC	-4.841029693	-27.67166667	5.716070428	0,43074	0.037460084
197	PA0182_at	PA0182 /DEF=probable short-chain dehydrogenase /F	-4.83770336	-31.82	6.577501272	0,45501	0.037460084
3904	PA3900_at	PA3900 /DEF=probable transmembrane sensor /FUNC	-4.831501746	-54.17666667	11.21321476	0,47957	0.037460084
4222	PA4225_pchF_at	PA4225 /GENE=pchF /DEF=pyochelin synthetase /FU	-4.829801061	-73.01833333	15.11829005	0,40684	0.037460084
5028	PA5033_at	PA5033 /DEF=hypothetical protein /FUNCTION=Hypo	-4.829148908	-43.685	9.046107468	0,43494	0.037460084
4040	PA4038_at	PA4038 /DEF=hypothetical protein /FUNCTION=Hypo	-4.817585886	-35.665	7.403085455	0,30287	0.037460084
5506	PA5512_at	PA5512 /DEF=probable two-component sensor /FUNC	-4.800200692	-51.66	10.76205003	0,47757	0.037460084
1078	PA1063_at	PA1063 /DEF=hypothetical protein /FUNCTION=Hypo	-4.793660836	-20.48	4.272308931	0,49420	0.037460084
5107	PA5112_estA_at	PA5112 /GENE=estA /DEF=esterase EstA /FUNCTION=	-4.782029739	-178.0983333	37.24325089	0,41237	0.037460084
4676	PA4680_at	PA4680 /DEF=hypothetical protein /FUNCTION=Hypo	-4.771167739	-68.875	14.43566937	0,26300	0.037460084
3411	PA3406_hasD_a	PA3406 /GENE=hasD /DEF=transport protein HasD /F	-4.767888109	-25.73666667	5.397917502	0,49460	0.037460084
3416	PA3411_r_at	PA3411 /DEF=hypothetical protein /FUNCTION=Hypo	-4.744949132	-43.365	9.139191758	0,46518	0.037460084
3258	PA3253_at	PA3253 /DEF=probable permease of ABC transporter	-4.733581549	-15.80333333	3.338557321	0,45165	0.037460084
2431	PA2424_at	PA2424 /DEF=probable non-ribosomal peptide synthe	-4.721021287	-30.71666667	6.506360552	0,44903	0.037460084
3666	PA3662_at	PA3662 /DEF=hypothetical protein /FUNCTION=Hypo	-4.655665277	-328.7116667	70.60466058	0,42056	0.037460084
5476	PA5482_at	PA5482 /DEF=hypothetical protein /FUNCTION=Hypo	-4.640093752	-820.9716667	176.9299739	0,44329	0.037460084
3990	PA3986_at	PA3986 /DEF=hypothetical protein /FUNCTION=Hypo	-4.636964666	-68.86833333	14.85202892	0,48386	0.037460084
1344	PA1329_at	PA1329 /DEF=conserved hypothetical protein /FUNCT	-4.62147377	-24.195	5.235342924	0,45466	0.037460084
4378	PA4382_at	PA4382 /DEF=hypothetical protein /FUNCTION=Hypo	-4.60804586	-46.01333333	9.985433029	0,34547	0.037460084
2072	PA2063_at	PA2063 /DEF=hypothetical protein /FUNCTION=Hypo	-4.590518742	-29.23833333	6.369287433	0,47779	0.037460084
2873	PA2868_i_at	PA2868 /DEF=hypothetical protein /FUNCTION=Hypo	-4.571843612	-65.42333333	14.31005495	0,27969	0.037460084
4361	PA4365_at	PA4365 /DEF=probable transporter /FUNCTION=Tran	-4.570911535	-22.21833333	4.860810182	0,48632	0.037460084
252	PA0237_at	PA0237 /DEF=probable oxidoreductase /FUNCTION=	-4.559389106	-141.5516667	31.04619136	0,32078	0.037460084
1191	PA1176_napF_at	PA1176 /GENE=napF /DEF=ferredoxin protein NapF /	-4.549881039	-25.17	5.532012768	0,41560	0.037460084
203	PA0188_at	PA0188 /DEF=hypothetical protein /FUNCTION=Hypo	-4.532799583	-93.23333333	20.5685982	0,31047	0.037460084
3534	PA3530_at	PA3530 /DEF=conserved hypothetical protein /FUNCT	-4.503474982	-457.4533333	101.577856	0,19188	0.037460084
2989	PA2984_at	PA2984 /DEF=hypothetical protein /FUNCTION=Hypo	-4.475526696	-46.34833333	10.35595059	0,37690	0.037460084
4777	PA4781_at	PA4781 /DEF=probable two-component response regu	-4.453347221	-78.78666667	17.6915616	0,45532	0.037460084
1205	PA1190_at	PA1190 /DEF=conserved hypothetical protein /FUNCT	-4.418944607	-338.9183333	76.69666933	0,21874	0.037460084
2524	PA2518_xylX_at	PA2518 /GENE=xylX /DEF=toluate 1,2-dioxygenase a	-4.416329387	-15.78333333	3.573857824	0,49461	0.037460084
5390	PA5396_at	PA5396 /DEF=hypothetical protein /FUNCTION=Hypo	-4.405424488	-237.6383333	53.94221011	0,16068	0.037460084
2320	PA2312_at	PA2312 /DEF=probable transcriptional regulator /FUN	-4.375992201	-39.10833333	8.937020802	0,41446	0.037460084
2514	PA2508_catC_at	PA2508 /GENE=catC /DEF=muconolactone delta-ison	-4.352795034	-569.7166667	130.8852501	0,05449	0.037460084
242	PA0227_at	PA0227 /DEF=probable CoA transferase, subunit B /F	-4.342094005	-178.02	40.99865175	0,15431	0.037460084
1705	PA1691_pscT_at	PA1691 /GENE=pscT /DEF=translocation protein in ty	-4.327892185	-17.89666667	4.135192353	0,48025	0.037460084

341	PA0326_at	PA0326 /DEF=probable ATP-binding component of A	-4.308092727	-76.91	17.85244768	0,42643	0.037460084
2688	PA2682_at	PA2682 /DEF=conserved hypothetical protein /FUNCT	-4.293944192	-83.915	19.54263871	0,42762	0.037460084
2519	PA2513_antB_at	PA2513 /GENE=antB /DEF=anthranilate dioxygenase	-4.279994809	-898.2133333	209.8631829	0,02397	0.037460084
4798	PA4803_at	PA4803 /DEF=hypothetical protein /FUNCTION=Hypo	-4.234850682	-44.85333333	10.5914793	0,48510	0.037460084
1915	PA1903_s_at	PA1903 /DEF=phenazine biosynthesis protein PhzE /F	-4.213002011	-47.42166667	11.25602754	0,46376	0.037460084
4030	PA4028_i_at	PA4028 /DEF=hypothetical protein /FUNCTION=Hypo	-4.208768474	-64.77666667	15.39088383	0,47300	0.037460084
4223	PA4226_pchE_at	PA4226 /GENE=pchE /DEF=dihydroaeruginosic acid sy	-4.178438956	-273.4033333	65.43193193	0,31811	0.037460084
4433	PA4437_at	PA4437 /DEF=hypothetical protein /FUNCTION=Hypo	-4.173985086	-40.21333333	9.634278156	0,49761	0.037460084
4903	PA4908_at	PA4908 /DEF=hypothetical protein /FUNCTION=Hypo	-4.145536941	-43.34833333	10.45662696	0,45258	0.037460084
2100	PA2091_at	PA2091 /DEF=hypothetical protein /FUNCTION=Hypo	-4.129487336	-59.40666667	14.38596654	0,43892	0.037460084
1862	PA1848_at	PA1848 /DEF=probable MFS transporter /FUNCTION=	-4.125317371	-21.54666667	5.223032492	0,47016	0.037460084
3994	PA3990_at	PA3990 /DEF=conserved hypothetical protein /FUNCT	-4.088011136	-36.02166667	8.811538293	0,47817	0.037460084
2087	PA2078_at	PA2078 /DEF=hypothetical protein /FUNCTION=Hypo	-4.072919929	-31.755	7.796617795	0,44299	0.037460084
4073	PA4071_at	PA4071 /DEF=hypothetical protein /FUNCTION=Hypo	-4.06659971	-29.57666667	7.272962794	0,48947	0.037460084
138	PA0123_at	PA0123 /DEF=probable transcriptional regulator /FUN	-4.061446667	-52.03	12.8107062	0,43261	0.037460084
2062	PA2053_cynT_at	PA2053 /GENE=cynT /DEF=carbonate dehydratase /F	-4.059213299	-55.67	13.7144801	0,30716	0.037460084
4376	PA4380_at	PA4380 /DEF=probable two-component sensor /FUNC	-4.048451762	-42.17166667	10.41673932	0,49525	0.037460084
5398	PA5404_at	PA5404 /DEF=hypothetical protein /FUNCTION=Hypo	-4.033798915	-19.58166667	4.854398318	0,49488	0.037460084
4084	PA4082_at	PA4082 /DEF=probable adhesin /FUNCTION=Motility	-4.018816418	-18.47	4.595880498	0,44390	0.037460084
326	PA0311_at	PA0311 /DEF=hypothetical protein /FUNCTION=Hypo	-3.986438652	-75.34	18.89907423	0,41050	0.037460084
5656	Pae_L81176cds6	L81176 /GENE= /PROD=unknown /FEATURE=cds6 /I	-3.982779833	-178.715	44.87192551	0,19345	0.037460084
3602	PA3598_at	PA3598 /DEF=conserved hypothetical protein /FUNCT	-3.973544237	-22.70166667	5.713203456	0,48035	0.037460084
1559	PA1545_at	PA1545 /DEF=hypothetical protein /FUNCTION=Hypo	-3.936337226	-52.835	13.42237643	0,21938	0.037460084
3713	PA3709_at	PA3709 /DEF=probable MFS transporter /FUNCTION=	-3.933973572	-43.465	11.04862532	0,47700	0.037460084
3054	PA3049_rmf_at	PA3049 /GENE=rmf /DEF=ribosome modulation factor	-3.915563317	-2962.338333	756.5548285	0,33850	0.037460084
1315	PA1300_at	PA1300 /DEF=probable sigma-70 factor, ECF subfami	-3.913884136	-29.7	7.588369754	0,45574	0.037460084
439	PA0424_mexR_at	PA0424 /GENE=mexR /DEF=multidrug resistance ope	-3.912345815	-88.415	22.59897366	0,44536	0.037460084
1913	PA1901_s_at	PA1901 /DEF=phenazine biosynthesis protein PhzC /F	-3.899484717	-78.58166667	20.15180784	0,40052	0.037460084
175	PA0160_at	PA0160 /DEF=hypothetical protein /FUNCTION=Hypo	-3.880017286	-40.58	10.45871629	0,46668	0.037460084
4213	PA4211_g_at	PA4211 /DEF=probable phenazine biosynthesis protei	-3.823166685	-21.05166667	5.506342882	0,41442	0.037460084
603	PA0588_at	PA0588 /DEF=conserved hypothetical protein /FUNCT	-3.757273623	-527.6783333	140.4418167	0,42421	0.037460084
5410	PA5416_soxB_at	PA5416 /GENE=soxB /DEF=sarcosine oxidase beta si	-3.696802159	-18.34666667	4.962847856	0,49597	0.037460084
176	PA0161_at	PA0161 /DEF=hypothetical protein /FUNCTION=Hypo	-3.695688889	-40.64	10.99659663	0,28501	0.037460084
249	PA0234_at	PA0234 /DEF=hypothetical protein /FUNCTION=Hypo	-3.652898389	-22.21	6.080103423	0,48860	0.037460084
2354	PA2347_at	PA2347 /DEF=hypothetical protein /FUNCTION=Putat	-3.596594006	-32.05833333	8.913525763	0,49833	0.037460084
5470	PA5476_citA_at	PA5476 /GENE=citA /DEF=citrate transporter /FUNCT	-3.586054696	-30.4	8.477282858	0,45743	0.037460084

5391	PA5397_at	PA5397 /DEF=hypothetical protein /FUNCTION=Hypo	-3.54873185	-58.95166667	16.61203753	0,42869	0.037460084
4152	PA4150_at	PA4150 /DEF=probable dehydrogenase E1 componen	-3.486481049	-146.6233333	42.05482011	0,33519	0.037460084
120	PA0105_coxB_at	PA0105 /GENE=coxB /DEF=cytochrome c oxidase, su	-3.454640684	-299.3266667	86.64480449	0,10418	0.037460084
243	PA0228_pcaF_at	PA0228 /GENE=pcaF /DEF=beta-ketoadipyl CoA thiol	-3.418453979	-61.25833333	17.91989411	0,25377	0.037460084
3911	PA3907_at	PA3907 /DEF=hypothetical protein /FUNCTION=Hypo	-3.41294465	-33.89333333	9.930818342	0,42453	0.037460084
5415	PA5421_fdhA_at	PA5421 /GENE=fdhA /DEF=glutathione-independent f	-3.317491273	-415.7983333	125.3351702	0,16083	0.037460084
4035	PA4033_at	PA4033 /DEF=hypothetical protein /FUNCTION=Hypo	-3.315756529	-27.645	8.337463791	0,36720	0.037460084
2518	PA2512_antA_at	PA2512 /GENE=antA /DEF=anthranilate dioxygenase	-3.299428314	-447.1383333	135.5199419	0,07694	0.037460084
4894	PA4899_at	PA4899 /DEF=probable aldehyde dehydrogenase /FU	-3.282694574	-57.45333333	17.50188208	0,49869	0.037460084
4350	PA4354_at	PA4354 /DEF=conserved hypothetical protein /FUNCT	-3.277015919	-40.91166667	12.4844272	0,47448	0.037460084
2942	PA2937_at	PA2937 /DEF=hypothetical protein /FUNCTION=Hypo	-3.249146215	-78.985	24.3094631	0,49645	0.037460084
338	PA0323_at	PA0323 /DEF=probable binding protein component of	-3.200224575	-13.42	4.193455704	0,49625	0.037460084
2513	PA2507_catA_at	PA2507 /GENE=catA /DEF=catechol 1,2-dioxygenase	-3.155677459	-874.29	277.0530294	0,03206	0.037460084
4566	PA4570_at	PA4570 /DEF=hypothetical protein /FUNCTION=Hypo	-3.071414883	-128.31	41.77553502	0,28217	0.037460084